

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 114883

TO: Jeffrey Parkin

Location: rem/3e39/3c18

**Art Unit: 1648** 

February 27, 2004

Case Serial Number: 09/891609

From: P. Sheppard

**Location: Remsen Building** 

Phone: (571) 272-2529

sheppard@uspto.gov

#### Search Notes

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#### **△3TIC-Biotech/ChemLib**

114883

From:

Parkin, Jeffrey

Sent:

Sunday, February 22, 2004 4:51 PM

To: Subject: STIC-Biotech/ChemLib U.S. Serial No. 09/891,609

Please search SEQ ID NOS.: 2 and 4 from the aforementioned application (09/891,609; Stamatatos et al.) v. all relevant databases, including interference. Please provide a paper copy and electronic copy of the results.

Thanks!

JSP AU 1648 REM 3E39 2-0908

Searcher:\_\_\_\_\_\_Phone:\_\_\_\_\_\_
Location:\_\_\_\_\_\_
Date Picked Up:\_\_\_\_\_\_
Date Completed:\_\_\_\_\_\_
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Online time:\_\_\_\_\_

| TYPE OF SEARCH: |
|-----------------|
| NA Sequences:   |
| AA Sequences:   |
| Structures:     |
| Bibliographic:  |
| Litigation:     |
| Full text:      |
| Patent Family:  |

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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HIV-1 gpl gp120 fro Amino aci

AAW43069 AAR67726 AAB85999

HTLV-III Lymphaden Modified

HIV prote Sequence HTLV-III Sequence

HIV-1 env Human lym HIV virus

Aar67726 Aab889999 Aar19389 Aar25940 Aar25940 Aap80966 Aap60422 Aap60422 Aap60422 Aap60422 Aap60322 Aap60332 Aap60332 Aap60053 Aap60053 Aap60053 Aab10053 Aab10053 Aab10053 Aab10053 Aab10053

AAR43869
AAO19389
AAO19389
AAP80966
AAP80966
AAP60349
AAP60349
AAW89325
AAW

Sequence Wild type Human imm HIV-1 coa HIV-1 env HIV 9941 HIV-1 NL4

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## ALIGNMENTS

1586107

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

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Minimum

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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Geneseq\_29Jan04:\*

Database

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\*

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geneseqp2004s:\*

1586107 segs, 282547505 residues

Modified full-length HIV-1 SF162DV2 gp140 envelope protein. â Human immunodeficiency virus 1; strain SF162 (clade /note= "Encoded by CAGCTC" Shrivastava I; (AARO-) AARON DIAMOND AIDS RES CENT. Location/Qualifiers Æ AAU75155 standard; protein; 646 27-JUN-2001; 2001WO-US020483. 27-JUN-2000; 2000US-0214608P. 26-JUN-2001; 2001US-00891609. Stamatatos L, Barnett S, (first entry) WPI; 2002-130836/17. N-PSDB; AAS15498. 539 Misc-difference WO200200250-A2 08-MAY-2002 03-JAN-2002 Synthetic AAU75155; 

> Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

Length DB Query Match Score Š.

Aay97073 Variant H Abr55684 HIV isola Abr55684 HIV isola Abb66555 Human imm Abb66211 HIV Env i Abb66211 HIV Env i Abb67724 9p120 fro Abr55495 Amino aci Abr55495 Amino aci Abr5739 HIV isote Aay77298 HIV-1 (AT Aay77298 HIV-1 (AT Abb67189 And Saso Abu67186 Env prote Abb67186 Env prote Abb67186 Env prote Aar29766 env gene Aar29766 env gene Aar29766 env gene env gene ARV-2 (9B Human Imm Env prote gp120 fro HIV-SF2 v Aaw11581 | Aaw88113 | Aar67725 | Aaw31284 | AAY97073 AAU75156 ABR55684 ADC13218 ABU66565 ABB06211 AAB82761 AAB855495 AAP80967 AAW53112 AAY77298 AAY77298 ABU57553 ABU57550 ABU63182 ABU63186 AAR29706 AAR29706 AAW11581 AAW88113 AAR67725 AAW31284 φ 3474 3422 3327 3327 3279.5 3274.5 3264.5 3065 3065 3006.5 Result

AAU75155

Human immunodeficiency virus type 1; HIV-1; gp140 envelope protein; second hypervariable region; V2; SF162deltaV2; SF162DV2; AIDS; acquired immunodeficiency syndrome; anti-HIV; mutant; mutein; immunogen.

Immunizing an animal and eliciting an immune response against heterologous HIV-1 in an animal, involves administering an immunogen comprising modified HIV-1 envelope protein, or DNA or virus encoding the protein.

Claim 5; Fig 16; 62pp; English.

The present invention relates to methods for immunising an animal, preferably human, against heterologous human immundeficiency virus type 1 (HIV-1), and eliciting a heterologous immune response to HIV-1 in that animal. The method comprises administering an immunogen having at least

envelope; Env;

modified;

HIV-1; vaccine; anti-HIV; immunogenic; modilied CD4 binding region; VI/V2 loop; bridging sheet. Human immunodeficiency virus 1; isolate SF162.

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one modified HIV-1 envelope protein with a deletion in the second modified HIV-1 region or its fragment, or DNA or virus encoding the modified HIV-1 envelope protein. The invention discloses the polymucleotide and amino acid sequences for the full-length HIV-1 explaintent of SF162DV2) gp140 envelope protein, and, for an N-terminal mutant of SF162DV2. The immunogens of the invention are useful for immunishing an animal against heterologous HIV-1 strains by eliciting neutralising antibodies or protective antibodies in the animal. The method can be used to treat acquired immunodeficiency syndrome (AIDS). The present sequence represents the full-length modified HIV-1 SF162DV2 gp140 envelope protein
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; Pred. No. 1.9e-169;
0; Mismatches 0;
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Best Local Similarity
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Novel modified HIV Env polypeptides useful as immunizing agents and for preparing a vaccine to elicit an immune response against a broad range of HIV subtypes.

ä Martin

Α,

Hartog

Barnett S,

(CHIR ) CHIRON CORP.

WPI; 2000-465745/40.

99WO-US031272. 98US-0114495P.

30-DEC-1999; 31-DEC-1998; 29-SEP-1999;

06-JUL-2000

WO200039303-A2

Claim 5; Page 115-117; 139pp; English.

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Novel immunogenic modified human immunodeficiency virus (HIV) envelope

(Env) polypeptides having an amino acid deleted or replaced in the region

corresponding to residues 420-436 or 119-123 and 199-210 relative to

isolate HXB-2 are disclosed. The modified Env polypeptide is based on HIV

strain SF162, with numbering relative to isolate HXB-2. The Env

carain SF162, with numbering relative to isolate HXB-2. The Env

polypeptides are modified Boo as to expose at least part of the CD4

binding region. The modified HIV Env polypeptides, coding polymucleotides

and constructs, further comprising an adjuvant, are used for inducing an

immune response in an individual. The method involves administering a

first composition comprising a polymucleotide encoding the Env

comprising a modified Env polypeptide as a booster in an amount

comprising a modified Env polypeptide as a booster in an amount

comprising a modified Env polypeptides can be used for a number of

intracellularly produced Env polypeptides can be used for a number of

diagnostic and therapeutic purposes to determine the presence of reactive

antibodies/and or Env proteins in a biological sample to aid in the

cinemunization. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DTEVHNVWATHACVPTDPNPQEIVLENVTENFNWWKNNWVEQMHEDIISLWDQSLKPCVK 120
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Pred. No. 1.1e-166;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.5%;
Best Local Similarity 95.4%;
Matches 643; Conservative (
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AAY97073 standard; protein; 847

Variant HIV-1 SF162 Env gp160.

(first entry)

(revised)

12-SEP-2003 31-OCT-2000

AAY97073;

AAY97073
ID AAY9
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AC AAY9
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DT 31-C
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DE Vari

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87 9 147 120 180

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327 300 387

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preferably human, against hererologous human immunodeficiency virus type 1 (HIV-1), and eliciting a heterologous immune response to HIV-1 in that animal. The method comprises administering an immunogen having at least one modified HIV-1 envelope protein with a deletion in the second hypervariable (V2) region or its fragment, or DNA or virus encoding the modified HIV-1 envelope protein. The invention discloses the polymucleotide and amino acid sequences for the full-length HIV-1 spridged tav2 (SF162DV2) gp140 envelope protein, and, for an N-terminal mutant of SF162DV2. The immunogens of the invention are useful for immunising an animal against heterologous HIV-1 strains by eliciting neutralising antibodies or protective antibodies in the animal. The method can be used to treat acquired immunodeficiency syndrome (AIDS). The present sequence represents the N-terminal mutant (deletion of amino acids 1-27) of modified HIV-1 SF162DV2 gp140 envelope protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VTENFNAMKONNYVEQMHEDIISLADQSLKPCVKLTPLCVTLHCTNLKOATNTKSSNWKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRGEIKNCSFKVGAGKLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGS
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    present invention relates to methods for immunising an animal,
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                                                                                                                                                                                                                                                                                   Length 619;
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100.0%; Pred. No. 5.8e-162;
ive 0; Mismatches 0;
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nes 619; Conservative
                                                                                                                                                                                                                                                      Sequence 619 AA;
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TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunizing an animal and eliciting an immune response against heterologous HIV-1 in an animal, involves administering an immunogen comprising modified HIV-1 envelope protein, or DNA or virus encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1; HIV-1; gpl40 envelope protein;
second hypervariable region; V2; SF162deltaV2; SF162DV2; AIDS;
acquired immunodeficiency syndrome; anti-HIV; mutant; mutein; immunogen.
                                                                                                                                                                                                          QQQNNLLRAIEAQEHLLQLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVP
                                                             SGGDPEIVMHSFNCGGBFFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEV
                                                                                                                                                                                                                                                    QQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVP
                   TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS
                                                                               361 SGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEV
                                                                                                                        GKAMYAPPIRGGIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYVVV
                                                                                                                                                                                        KIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIV
                                                                                                                                                                                                                                                                                                                  WNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal mutant of modified HIV-1 SF162DV2 gp140 envelope protein.
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26-JUN-2001; 2001US-00891609.
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                                                                                                                                                                                                                                                                                                                                                                               WNWPDISKWLWYIK 646
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N-PSDB; AAS15499.
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Misc-difference
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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Env, Int. Nef, plSRnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscularly, intranssally, intravaginally, intravectally, orally or intravenously. The expression cassette is useful for immunisation, generating packaging cell lines and producing HIV polypeptides. This sequence represents an HIV Type C related protein of
                                                                                                                                             552
                                                                                                                                                                                   589
FFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV Gag; Env; Int; Nef; pl5RnaseH; Pol; Tat; Prot; b therapy; vaccine; immunisation; HIV.
                                                                                                                                                                                                                                                         TWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                                                                                                                                             699
                                                        QREKRAVILGAMFLGFLGAAGSIMGARSLILITVQARQLLSGIVQQQNNLLRAIEAQQHLL
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                                     NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV
                                                                                                             OREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSG1VQQQNNLLRA1EAQQHLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide including an HIV Gag, Env. Int. Nef, pisRnaseH, Pol. Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Length 842;
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                                                                                                                                                                                                                                                                                                                                                                                        ADC13218 standard; protein; 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rev; HIV type C; gene therapy;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New expression cassettes and polynucleotides encoding HIV Gag, Nef, Prot, Tat, Rev, Vif, Vpr, Vpu, or Env polypeptides, useful for DNA immunization or generating an immune response against HIV in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Nef, Prot, Tar, Nev, Vif, Wr, Vpu, or Env polypeptide. The expression cassettes, HIV polypeptides and polynucleotides encoding the HIV polypeptides and polynucleotides encoding the HIV polypeptides and polynucleotides are also useful for generating packaging cell lines or producing the HIV polypeptides. Sequences ABR55684-688 represent env polypeptides from various HIV isolates. (Updated on 23-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTKSSNWKEMDRGEIKNCSFKVGAG--------KLINCNTS 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNPQEIVLENVTENFNWWKDNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT
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                                                                                            prot; tat; rev; vif; vpr; vpu; env; anti-HIV; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3279.5; DB 6;
Pred. No. 1.9e-159;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                          ;;
;;
                                                        HIV isolate SF162 env polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 2A-C; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                          Lian
                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.2%;
Matches 619; Conservative
                                                                                                                                                                                                                                                                                               31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349728P.
                                                                                                                                                                                                                                                             05-JUL-2002; 2002WO-US021342
                                                                                                                                                                                                                                                                                                                                                                                          SW,
                      (first entry)
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                                                                                                                                                                                       WO2003020876-A2
                                                                                                                   response
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   23-OCT-2003
18-AUG-2003
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                                                                                                                               PNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM 589
                                                                                            72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 646
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                                                                                                                                                                                                                                                                                                                                                                                               LINGSLAEEGVVIRSENFIDNAKTIIVOLKESVEINCTRPNNNTRKSITIGPGRAFYATG
                                                                              LLLGMLMIC-SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD
                                                                                                                                                      PNPQEIVLENVTENFNWWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT
                                                                                                                                                                                                         NTKSSNWKEMDRGEIKNCSFKVGAG------KLINCNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 FFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NITGLLLTRDGGKEISNTTEIFRPGGCDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV
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                                                                                                                                                                                                                                                                                                                     193 VITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQL
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                     Gaps
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                   Indels
ed. No. 1.9e-159;
Mismatches 7;
   Pred.
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               5.7
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94.28;
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                   Conservative
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                                                                                                                                                                                                                                                               New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This is the amino acid sequence of a human immunodeficiency virus (HIV) envelope (env) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 PNPQEIVLENVTENFNAMKONNWVEQMHEDIISLMDQSLKPCVKLTPLCTVLKONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIIGDIRQAHCNISGEKWNWTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLINCNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTKSSNWKEMDRGEIKOCSFKVTTSIRNKMQKEYALFYKLDVVPIDNDNTSYKLINCNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DI IGDIRQAHCNI SGEKWINTLKQI VTKLQAQFGNKTI VFKQSSGGDPEI VMHSFNCGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGMLMIC-SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLNGSLABEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NITGLLLTRDGGKEISNTTEIFRPGGDMRDNWRSELYKYKVVKTEPLGVAPTKAKRRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITQACPKVSFEP1P1HYCAPAGFA1LKCNDKKFNGSGPCTNVSTVQCTHG1RPVVSTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9
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8
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Pred. No. 3.5e-159;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTKSSNWKEMDRGEIKNCSFKVGAG----
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2A-C; 262pp; English
                                                                                                                                                                  Lian Y;
16-JAN-2002; 2002US-0349728P.
16-JAN-2002; 2002US-0349793P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.3%;
94.1%;
                                                                                                                                                                  SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 94.1
nes 618; Conservative
                                                                                                                                                                  Zur Megede J, Barnett
                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                      WPI; 2003-221602/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 842 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531
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Preparing an ancestral viral amino acid sequence useful as a vaccine comprises determining a recent ancestor of a circulating virus by maximum likelihood phylogeny analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                        QREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                 NTKSSNWKEMDRGEIKNCSFKVTTSIRNKMOKEYALFYKLDVVPIDNDNTSYKLINCNTS
                                                                 LLNGSLABEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATG
                                                                                                                                       DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
                                                                                                                                                                                                     DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
                                                                                                                                                                                                                                                   FFYCUSTOLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
                                                                                                                                                                                                                                                                      NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV
                                                                                                                                                                                                                                                                                                                                                                                       QREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM
                                                  VITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of an ancestral HIV-1 group M, subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1; env gene; gp160 protein; ancestral gene; phylogeny; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancestral HIV-1 group M, subtype B gp160 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 다.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB82761 standard; protein; 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
 16-FEB-2001; 2001WO-US005288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000; 2000US-0183659P
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N-PSDB; AAH26468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2003
29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82761;
                                                                                 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes expression cassettes comprising a polymucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polymucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins The polymucleotides are particularly useful in gene Herapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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72
                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy.
                                                  LLCGAVEVSPSAVEKLMVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNPQEIVLENVTENVTENFNWKNNMVEQMHEDIISLWDQSLKPCCVKLTPLCVTLHCTNLKNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNPOBIVLENVTENFUMWKNNMVBQMHBDIISLWDQSLKPCVKLTPLCVTLHCTNLKNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLGMLMIC-SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%; Score 3264.5; DB 5;
llarity 93.8%; Pred. No. 1.1e-158;
Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                                                                                                                                                                                                                                                       HIV Env isolate SF162 amino acid seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engelbrecht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 NTKSSNWKEMDRGEIKNCSFKVGAG---
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                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus; type
                                                                                                                                                                      ABB06211 standard; protein; 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2000; 2000US-00610313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001; 2001WO-US021241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SW,
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
(UYST-) UNIV STELLENBOSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zur Megede J, Barnett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 842 AA;
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Best Local Simi
Matches 616;
                                                                                                                                                                                                                                      15-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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cc gp160 (env gene product) sequence. The invention provides compositions and methods for determining ancestral viral gene sequences and ancestral viral protein sequences for highly diverse viruses, such as HIV-1. The methods use samples of circulating viruses to determine an ancestral viral sequence by maximum likelihood phylogeny analysis. In the present case, the ancestral HIV-1 subtype B env sequence (see AAN26468) was determined using 38 subtype B sequences (obtained from 9 different countries) and 3 subtype D (outgroup) sequences. The distances between this ancestral viral sequence and circulating strains used to determine ti were on average 12.3% (range: 8.0-21.0%) while the available specimens were 17.3% different from each other (range: 13.3-23.2%). Thus, the ancestral force sequence was, on average, more closely related to any given circulating virus than to any other variant. The ancestral gp160 sequence included a wide variety of immunogenically active peptides when processed for antigen presentation; nearly all known subtype B CTL epitope consensus amino acids wer represented Thus, an immunogenic composition to this subtype B ancestor protein will elicit broad neutralising antibody against HIV-1 isolates of the same subtype, and will also elicit a broad cellular response mediated by antigen-specific T-cells. A claimed vaccine composition comprises a viral ancestor protein or its immunogenic fragment, especially one derived from the HIV-1 group M subtype B gp160 ancestral protein. (Updated on 11-SEP-2003 to standardise OS field) DTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120 61 DTEVHNVWATHACVPTDPNPQEVVLENVTENFNWMKNNWVEQMHEDIISLWDQSLKPCVK 120 162 194 254 241 AILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTDNAKT 300 361 IVTKLREQFGNNKTTIVFNQSSGGDPEIVMHSFNCGGEPFYCNSTQLFNSTWHFNGTWGN 420 421 477 255 IIVQLKESVEINCTRPNNVTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQ 314 315 IVTKLQAQFGNK--TIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGP 370 9 9 181 QKEYALFYKLDVVPIDNDNNNTNNNTSYRLINCNTSVITQACPKVSFEPIPIHYCTPAGF NNT-----NGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDG 1 MRVKGIRKNYQHLWRWGTMLLGMLMICSAAEKLWVTVYYGVPVWKEATTTLFCASDAKAY 1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKBATTTLFCASDAKAY LTPLCVTLHCTN--LKNATNTKSSN------WKEMDRGEIKNCSFKVGAG----AILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKT G--KEISNT-TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVVQREKRAV-Gaps -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGF 64; Length 883; Indels 35; Query Match

88.2%; Score 3065; DB 4;
Best Local Similarity 83.7%; Pred. No. 1.7e-148;
Matches 594; Conservative 17; Mismatches 35; -----Sequence 883 AA; 195 371 61 121 422 163

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This protein is the gpl20 (envelope glycoprotein) from the GNEB isolate of HIV-1 (human immunodeficiency virus type 1). There are neutralising epitopes in the V2 and C4 domains of gpl20, in addition to the neutralising epitopes in the V3 domain. Although the amino acid sequences of the neutralising epitopes in the V2 v4 and C4 domains are variable, the amount of variation is highly constrained. This facilitates the design of HIV subunit vaccines that can induce antibodies that neutralise the most common HIV strains for a given geographic region. This invention provides a multivalent gpl20 subunit vaccine where the gpl20 present in the vaccine is from at least two HIV isolates which have different amino acid sequences for a neutralising epitope in these regions. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field) DTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120 61 DIEVHNVWATHACVPTDPNPQEIGLENVTENFNWKNNWVEQMHEDIISLWDQSLKPCVK 120 162 9 MIVKGIRKNCQHLWRWGTMLLGMLMICSAAEKLWVTVYYGVPVWKEATTTLFCASDAKAY LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG--------1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY Gaps HIV; human immunodeficiency virus; gp120; glycoprotein; GNE clone; Use of HIV gp 120 polypeptide(s) - for developing probes for the analysis, prevention and therapy of HIV infection. 37; Length 850; BIDNYTGLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDITNWLWYIK 597 EIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK Indels DB 2; Claim 23; Page 27-30; 108pp; English. Ź gp120 from the HIV GNE8 isolate. AAR67724 standard; protein; 850 Human immunodeficiency virus 1. 94WO-US006036 93US-00072833 (first entry) Conservative Nakamura GR; (revised) (GETH ) GENENTECH INC. WPI; 1995-036112/05. Similarity N-PSDB; AAQ76018 Sequence 850 AA; isolate. 07-JUN-1994; 07-JUN-1993; WO9428929-A1 22-DEC-1994. 16-OCT-2003 25-MAR-2003 07-SEP-1995 Berman PW, 580; AAR67724; Н 661 61 121 Query Match Local Matches GNEB AAR67724 ID AAR RESULT ò g 8 셤 ò d ò 셤

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K-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWER

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481 GNNENTNNTDTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVG

478 TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGI

541 MLGAMFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGI

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The specification describes a method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a substitutions. The method comprises typing all individuals of a substitutions. The method is all individuals of a selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit pathogenic traits in a host, such as bacteria, fungi, mycobacterium, ciruse-like particles; for examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the hepatitis related viruses such as HCV and HBV. The method is useful for hepatitis related viruses such as HCV and HBV. The method is useful for cening a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism where the drug affects the replication of the microorganism at the cule care amino acid level. The present sequence represents a HIV envelope protein, which is expected to provide optimal cyctoxic T lymphocyte (CTL) induced therapeutic protection to the cohort examined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AKAYDTEVHNVWATHACVPTDPNPQEIVLENVTENFNWWKNNMVEQMHEDIISLWDQSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLNESVEINCT
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                                                                                                                                                                                                                                                                                                                                                                                            1 MRVKGIRKNYQHL----WRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCVKLTPLCVTLHCTNLKNATNT-KSSNWKEMDRGEIKNCSFKVGAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLIRDGGKEISNTTEIFRPGGGDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLTVQARQLLSGIVQQQNNLLRAIBAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGI
                                                                                                                                                                                                                                                                                                                                    6; Length 856;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                   86.5%; Score 3006.5; DB 6
84.2%; Pred. No. 1.6e-145;
ive 27; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                    478 YKYKVVKIEPLGVAPTKAKRRVMQREKRAVGIGAVFLGFLGAAGSTMGAASVTLTVQARL
                                                                                                                                                                                                                                                                                                                        YKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
                                                                                                                                     TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDNDNTSYRLISCNTSVITQACPKVSFBPIPIHYCAPAGFAILKCRDKKFNGTGPCTNV
                                                                                           LLSGIVQQQNNLLRAIEAEQHLLQLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLI
                                                                          STVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNN
                                                                                                                                                                                                 SGGDPEIVMHSFNCGGEFFYCNSTQLFNS-----TWNNTIGPNNTNGTITLPCRIKQII
                                                                                                                                                                                                                                                           NRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic marker; host response; HIV; AIDS related virus; vaccine; hepatitis related virus; HCV; HBV; drug resistance; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of a HIV envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR55495 standard; protein;
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ARV-2; enhanced promoter; gene expression; cytomegalovirus; HIV; AIDS;
                                                                                                                                                                                                478 LYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLGFLGAAGSTWGAASMTLTVQAR
                                                                                                                                                                                                                                                         269 RPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTI
                                                                          358 VFISSSGGDPEIVLHSFNCGGEFFYCNTTQLFNSTWNSTEGSNNTGGNDTITLPCRIKQI
                                                                                                                                                                                                                                          QLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKL
                                                                                                                                                                                                                                                                                                     566 ICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLE
                 298 RPNNNTRKSITKGPGRVIYATGQIIGDIRKAHCNLSRAQWNNTLKQVVTKLREQPDNKTI
                                                          329 VFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNTNG--TITLPCRIKQI
                                                                                                                                                                              447 LYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enhanced promoter for gene expression - comprising cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the ENV protein contained in a complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENV protein contained in a complete ARV-2 nucleotide sequence.
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85US-00696534.
85US-00173447.
87US-0013894.
92US-00931191.
93US-00107377.
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24-DEC-1987;
17-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003
25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENV protein.
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17-AUG-1993;
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                                                                                                                      387
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AAW53112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of recombinant HIV envelope proteins in insect cells - useful as vaccine against AIDS and for diagnosis and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 KLDIIPIDNDTTSYTLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVKGIRKNYQHL----WRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.3%; Score 2997; DB 1; Length 851; 83.0%; Pred. No. 4.9e-145; Live 40; Mismatches 38; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Jellis CL;
                                                                                                                                                                                                         HIV; HT6; gp160; envelope protein; RF; AIDS.
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                                                                                                                                                                                                                                         Human immunodeficiency virus; variant RF
                                                                                                                                                                                                                                                                                                                                                                                                                                         Putney
                                                        AAP80967 standard; protein; 851 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page ?; 4pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Carson H,
                                                                                                                                                                                                                                                                                                                                                            86US-00941111.
87US-00091481.
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.0
nes 565; Conservative
                                                                                                                   (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                           (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-176944/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rusche J, Lynn D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN80948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 851 AA;
                                                                                                                                                                              HIV protein HT6
                                                                                                                                                                                                                                                                                                                                 14-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1987;
                                                                                                                   24-OCT-2003
25-MAR-2003
                                                                                                                                               15-NOV-1990
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Best Local Si
Matches 565;
                                                                                      AAP80967;
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셤 8 셤 HIV-1; immunoassay; antigen; pol fragment; p31; recombinant; antibody; detection; env protein.

CRL 8597) env protein.

HIV-1 (ATCC

(first entry) (revised)

12-SEP-2003 22-MAY-2000

AAY77298;

8597

Human immunodeficiency virus 1; 'ATCC CRL

US6013432-A.

85US-00696534. 85US-00773447. 87US-00138894. 92US-00931154.

30-JAN-1985; 06-SEP-1985; 24-DEC-1987;

31-OCT-1984;

CORP.

(CHIR ) CHIRON

08-JUL-1993;

17-AUG-1992

2000-170256/15 Luciw PA, Dina D;

95US-00443434 84US-00667501

17-MAY-1995;

11-JAN-2000

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nucleotide sequence of ARV-2 derived from partial sequences of several ARV clones. The invention provides a method for construction of a vector for expression of a polypeptide in a mammalian cell, comprising a polypeptide coding sequence operably linked downstream of an enhanced promoter comprises the human cytomegalovirus immediate early region (HCMV IRI) promoter and the first intron proximate to the 3' end of the HCMV IRI promoter. The polypeptide can be any of the HIV recombinant polypeptides and especially HIV gpl20. Expression of HIV gpl20 by COS 7 cells transfected with pCMV6a containing the gpl20 coding region, where pCMV6a is a vector containing the above enhanced promoter, is increased by a factor of 50-100 compared with the use of a vector containing the SV40 early promoter. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                   DIEVHNVWATHACVPTDPNPQEVVLGNVTENFNWWKNNWVEQMQEDIISLWDQSLKPCVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG------------ 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PCTNVSTVQCTHGIRPIVSTQLLLNGSLABEEVVIRSDNFTNNAKTIIVQLNESVAINCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGPNNTNGTITLPCRIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARQLESGIVQQQNNLERAIEAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLICTTAVPWNASWKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQEL
                                                                                                                                                                                                                                                                                                                                                  -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCT
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                 85.9%; Score 2984; DB 2; Length 855; ilarity 82.4%; Pred. No. 2.2e-144; Conservative 34; Mismatches 48; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LELDKWASLWNWFDISKWLWYIK 646
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Matches 563; Conserv
                                                                                                                                                                                                                                    Sequence 855 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 PIDNASTTINYTNYRLIHCNRSVITQACPKVSFEPIPIHYCTPAGFAILKCNNKTFNGKG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoassay for antibodies against human immune deficiency virus, for diagnosing infection, uses an immunogenic fragment of the pol protein as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIEVHNVWATHACVPTDPNPQEIVLENVTENFNWKNNMVEQMHEDIISLWDQSLKPCVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.9%; Score 2984; DB 3;
82.4%; Pred. No. 2.2e-144;
ive 34; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 4K-O; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 82.4%
Matches 563; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 855 AA;
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standard; protein; 855

AAY77298

RESULT 13 AAY77298 ID AAY7 XX

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The invention relates to the improvement of HIV-1 immunoassays by the use of an HIV-1 antigen comprising an immunogenic fragment of recombinant or between a BSTAI antigen comprising an immunogenic fragment of recombinant or between a BSTAI restriction site at position 3006 and an Ndel site at position 5131 of the genome (the proviral DNA sequence is given in AAZ90201). The immunogenic pol fragment is not immunologically cross-reactive with human T cell lymphotropic viruses I or II. The invention also encompasses the used of p31 as an antigen. The recombinant antigens may be produced in Bscherichia coli, Saccharomyces cerevisiae or in mammalian cells. Immunoassays using the recombinant HIV proteins may be used to diagnose and stage HIV-1 infections. Sequences AAY77300-X77302 represent, respectively, the gag, pol and env proteins encoded by the proviral DNA of a single isolate of HIV-1 (ATCC CRL 8597). (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                         DIEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFG-NKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGPNNTNGTITLPCRIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARQLISGIVQQQNNLIRAIEAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQEL
                                                                                                                                                                                                                                                                                            LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRS
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                                                                                                                                                                                                                                                                               MRVKGIRKNYQHLWRGGTLLLGMIMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                                                                                                                                   Length 855
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                               85.9%; Score 2984; DB 3;
82.4%; Pred. No. 2.2e-144;
ive 34; Mismatches 48;
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                                                                                                                                                                                                                                                        Matches 563; Conservative
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                           Sequence 855 AA;
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                                                                                                    IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGPNNTNGTITLPCRIKQ
                                                                                                                                                                                                                                            ARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pol fragment; p31; recombinant; antibody;
                    ELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQ
                                                                                                                                                                                                          KLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEBSQNQQEKNEQEL
                                                                                                                                                 IINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRS
                                                                                                                                                                                                                                                         ARQLISGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSG
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85US-00696534.
85US-00173447.
87US-00138894.
92US-00931154.
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(first entry)
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N-PSDB; AAZ90202.
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22-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
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                                                                                                                           antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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                                                                                                                       Immunoassay; human immunodeficiency virus; HIV; antibody; gag an aquired immunodeficiency syndrome; AIDS; HIV infection; vaccine; gene therapy; protein expression system; ARV-2; AIDS associated retrovirus 2.
                                                                                                                                                                                                                                                                                                                                                                                          George-Nascimento
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                                                                                                 AIDS associated retrovirus-2 (9B) (ARV-2 (9B)) ENV protein.
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Barr PJ,
                        standard; protein; 855 AA
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85US-00696534.
85US-00773447.
87US-00138894.
92US-00931191.
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Hallewell R, Bar
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Matches 563; Conservative
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06-SEP-1985;
24-DEC-1987;
17-AUG-1992;
                                                                                                                                                                                                                US6458527-B1
                                                                                                                                                                                       Retroviridae
                                                                                                                                                                                                                                                              28-JUN-1993;
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- KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSG
                                                                            PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCT
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1 MRVKGIRKOYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-193-2000
TELEPAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 850 amino acids
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
US-08-448-603A-28
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MEDIUM TYPE: Diskett
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
         5.1.6
Compugen Ltd
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5-08-482-847-14
5-07-956-483-10
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S-08-472-240A-7
S-08-817-441-103
S-08-817-440-103
S-07-956-483-16
S-07-916-098A-2
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US-07-956-483-14
US-08-388-809-6
US-08-388-809-6
US-08-48-803-15
US-08-488-803-15
US-09-134-075-30
US-09-134-075-30
US-09-134-075-30
US-09-134-075-30
US-09-134-075-30
US-09-134-075-30
US-09-134-075-30
US-09-134-900-9
US-09-134-900-9
US-09-134-900-9
US-08-463-028-11
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                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-448-603A-28
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3-09-718-096-23
3-08-788-815-7
                                                                                                                                                                            389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
         GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                        US-09-891-609A-2
3474
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Match Length
                  Copyright
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Perfect score:
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                                               OM protein
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Maximum DB
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                      Sequence 11,
Sequence 10,
Sequence 2, P
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Sequence 2, P
Sequence 11,
Sequence 6, P
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/08448603A; Sequence 28, Application US/08448603A; Sequence 28, Application US/08448603A; Betent No. 5864027; GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,603A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/072,833
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
US-09-157-963-7

US-09-337-387-11

US-08-172-240A-10

US-08-647-714-2

US-08-647-714-2

US-08-647-714-2

US-08-647-714-3

US-08-138-809-4

US-08-138-809-4

US-09-337-387-3

US-09-337-387-3

US-09-337-387-3

US-08-337-387-3

US-08-337-340A-1

US-08-337-340A-2

US-08-448-603A-3

US-08-448-603A-3

US-08-448-603A-3

US-08-448-603A-3

US-08-448-603A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGDPEIVMHSFNCGGEFFYCNSTQLFNS-----TWNNTIGPNNTNGTITLPCRIKQII 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 NAWQEVGKAMYAPPIRGQIRCSSNITGLLITRDGGN--NSFTEIFRPGGGDMRDNWRSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 NRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL
                                                                                                                                                                                                                                                                                                                                                                       1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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                                                                                                                                                                                                                                                                                                         Length 850;
                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                         DB 3;
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 APPLICATION NUMBER: 08/448,603
                           ATTORNEY AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 149:
TELECOWNUNICATION INFORMATION:
TELEPHONE: 415-393-2286
                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
                                                                                                                                                                                                                                                                                                                        Best Local Similary,
Matches 580; Conservative
                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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US-09-134-075-28
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US-09-492-739-28
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                                    DIEVHNVWATHACVPIDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
                                                      DIEVHNYWATHACYPTDPNPOEIGLENTENFINMKNNWVEOMHEDIISLWDOSLKPCVK 120
                                                                                                     LTPLCVTLHCTNLKNATNTKSSNWKEMDRGE1KNCSFKVGAG-------------------162
                                                                                                                      241 STVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFSDNAKTIIVQLNESVEINCTRPNNN 300
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                                                                                                                                                                      301 TRRSIHIGPGRAFYATGEIIGDIRQAHCNLSSTKWNNTLKQIVTKLREHF-NKTIVFNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 YKYKVVKIEPLGVAPTKAKRRVMQREKRAVGIGAVFLGFLGAAGSTMGAASVTLTVQARL
                                                                                                                                                                                                                                    STVQCTHGIRPVVSTQLLLAGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNN
                                                                                                                                                                                                                                                                                                         TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                          NRWQEVGKAMYAPPIRGQIRCSSNITGLLLIRDGGKEISNTTEIFRPGGGDMRDNWRSEL
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1 MIVKGIRKNCQHLWRWGTMLLGMLMICSAAEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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Sequence 28, Application US/09134075
Sequence 28, Application US/09134075
Sequence 28, Application US/09134075
Sequence 28, Application
APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
TITLE OF INVENTION: HIV Envelope
STREE: 3 Embarcadero Center
CITY: San Francisco
CITY: San Francisco
STREE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: SeatSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/134,075
FILING DATE:
FRIOR APPLICATION:
PRIOR APPLICATION DATA:
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US-09-134-075-28
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                                                                  420 NWWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGN--NSETEIFRPGGGDMRDNWRSEL 477
                                                                                                                                                                                                                                                                                 CTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLEL 626
                                                                                                                        YKYKVVKI EPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
                                                                                                                                                                                                    LLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLI
                                                                                                                                                                                                                             NRWQEVGKAMYAPPIRGQIRCSSNITGLLITRDGGKEISNTTBIFRPGGGDMRDNWRSEL
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83.0%; Pred. No. 2.2e-239;
tive 34; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     017753-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/07956483
Patent No. 6261799
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HYBRID, SO
TITLE OF INVENTION: gpl60 VARIANT
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: R 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               DKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 855 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
: United States
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Best Local Similarity 83.04
Matches 568; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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US-07-956-483-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DTEVHNVWATHACVPTDPNPOEIGLENDYTENPNWWKNNWVGOMHEDIISLWDOSLKPCVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 STVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFSDNAKTIIVQLNESVEINCTRPNNN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 SGGDPEIVMHSFNCGGEFFYCNSTQLFNS-----TWNNTIGPNNTNGTITLPCRIKQII 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATT1
                                                                                                                                                               Brown & Enersen, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATINE SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                            APPLICANT: Berman, Phillip W.
Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

88.2%; Score 3062.5; DB 4
Best Local Similarity 85.3%; Pred. No. 9.1e-245;
Matches 580; Conservative 28; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR DATE: 27-Jan-2000
CLASSIFICATION NUMBER: US/09/492,739
FILING DATE: 27-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/134,075
FILING DATE: <Unknown>
ATTORNEY,AGENT INPORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-492-739-28
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ADDRESSE: McCutchen, Doyle,
STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: CA
quence 28, Application US/09492739
tent No. 6331404
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 850 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                       COUNTRY: USA
    Sequence 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                  #1.25
                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: 8Cott, Watson T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGIOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; Score 2978.5; DB 1
82.3%; Pred. No. 8.2e-238;
tive 36; Mismatches 48;
                                                  Version
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,835
                                                                                                                                                                                                                                                                   TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.39
Matches 561; Conservative
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                                                                                                                                                    LTPLCVTLHCTNLK-----NATNTKSSNWKEMDRGEIKNCSFKVGAG------- 162
                                                                                   DIEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
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                                                                                                                                                                                                                                         KLDVVPIDNTSYTLINCNTSVITQACPKVSFEPIPIHYCA-RWFAILNCNNKKFNGTGPC
                                                                                                                                                                                                                                                                                        INVSTVOCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRP
                                                                                                                                                                                                                                                                                                         240 TNVSTVQCTHGIRPVVSTHLLLNGSLAEEEVVLRSENFTDNAKTIIVQLKEAVEINCTRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                      NNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNT----TEIFRPGGGDMRDNWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTV
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Bleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIPT: 20036-5601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08022835
Patent No. 5420030
GENERAL INFORMATION:
APPLICANT: Reitz Jr., Marvin S.
APPLICANT: Markham, Phillip D.
APPLICANT: Markham, Phillip D.
APPLICANT: Lori, Franco C.
APPLICANT: Lori, Franco C.
APPLICANT: Gallo, Robert C.
APPLICANT: Gallo, Robert C.
APPLICANT: Gallo, Robert C.
APPLICANT: Gallo, Robert C.
APPLICANT: Garner, Suzanne
APPLICANT: Garner, Suzanne
TITLE OF INVENTION: THEREOF
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US-08-022-835-6
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241 GPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFADNAKVIIVQLNESVEINC 300
                                                                                                                                                         361 IVFKHSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWNVTEESNNTVENNTILLPCRIKQ 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGK 564
                                                                                                                                                                                                                                                                                                                                421 IINMWQEVGRAMYAPPIRGQIRCSSNITGLLLTRDGGPE-DNKTEVPRPGGGDMRDNWRS
                                                                                                                                                                                                                                                                                                                                                                                                                         480 ELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAAAMTLTVQA
                                                                                                                                TRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 RLLLSGIVQQQNNLLRAIBAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
APPLICANT: GENOVEPFA; MARKHAM, PHILIP D. GALLO, ROBERT
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
APPLICANT: GRATHER, SIZANNE
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4092US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/647,714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLOPPY DISK, 3.5"
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08647714 Patent No. 5869313 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 345 PARK AVENUE
CITY: NEW YORK
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-647-714-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LTPLCVTLHCTNLKNATNTKSSNWKEMDR----GEIKNCSFKVGAG---
                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,

APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT

APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT

APPLICANT: GARTNER, SUZANNE

TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFILING DATE: 12-FEB-1535
APPLICATION DATA:
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/ACENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
FREFERENCE/DOCKET NUMBER: 2026-4092USZ
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: RLOPPY DISK, 3.5"
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
                                          625 ELDKWASLWNWFDISKWLWYIK 646
                                                                 Sequence 6, Application US/08388809
Patent No. 5576000
                                                                                                                                                                                                                                                                                                                                                                                                                                        FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORGAN & FINNER
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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INPORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
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MOLECULE TYPE: protein
US-08-388-809-6
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US-08-388-809-6
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                                                                                                                                                                                                                                    1 MRVTEIRKSYQHWWRWGIMLLGILMICNAEEKLWVTVYYGVPVWKEATTTLFCASDRKAY
                                                                                                                                                                                          Gaps
                                                                                                                                                                                          37;
                                                                                                                                                                DB 2; Length 855;
                                                                                                                                                                                                                                                                                                                              LTPLCVTLHCTNLKNATNTKSSNWKEMDR----GEIKNCSFKVGAG--
                                                                                                                                                                                          Indels
                                                                                                                                                                                           48;
                                                                                                                                                               85.7%; Score 2978.5; DB 2
82.3%; Pred. No. 8.2e-238;
ive 36; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELDKWASLWNWFDISKWLWYIK 646
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                                    TELEX: 421792
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 855 amino acids TYPE: amino acid
              (212) 758-4800
(212) 751-6849
                                                                                                                                                                           Best Local Similarity 82.3
Matches 561; Conservative
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
            TELEPHONE:
                          TELEFAX:
                                                                                                                                    US-08-647-714-6
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181 PIDNASTTTNYTNYRLIHCNRSVITQACPKVSPEPIPIHYCTPAGFAILKCNNKTFNGKG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 IVFNQSSGGDPEIVMHSFNCRGEFFYCNTTQLFNNTWRLNHTEGTKG-NDTILLPCRIKQ 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRS 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 PCTNVSTVQCTHGIRPVVSTQLLLMGSLAEBGVVIRSENFTDNAKTIIVQLKESVEINCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG-----
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                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 85.7%; Score 2976; DB 3; Best Local Similarity 82.3%; Pred. No. 1.3e-237; Matches 562; Conservative 34; Mismatches 49;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Peury, Sharon E
NEGISTRATION NUMBER: 36,113
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
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TOPOLOGY: lin
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Sequence 15, Application US/07956483
Patent No. 6261799
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: gp160 VARIANT

US-07-956-483-15

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181 PIDDDDRNSTRNSTNYRLISCNTSVITQACPKVSFEPIPIHFCTPAGFALLKCNNKTFNG 240
                                                       SGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEGEVVIRSENFTNNAKTIIVQLTEPVKIN 300
   DTEIHNVWATHACVPTDPNPQEVVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
                                                                                                                                                                        SGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEIN 266
                                                                                                                                                                                                                                             CTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNK 326
                                                                                                                                                                                                                                                                  TIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNT----NGTITLPCR 382
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                                   LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG-
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Patent No. 6042836
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLF
STREET: 3 Embarcadero Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,075 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,603
FILING DATE:
FILING DATE:
APPLICATION INFORMATION:
RILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halidav. Fm.1.
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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STATE: CA
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US-09-134-075-30
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                                                                                                  505 ARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSG 563
                                                                                                                                                                       KLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQEL 623
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                                BLYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQ
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; Patent No. 5864027
; GENERAL INFORMATION:
    APPLICANT: Berman, Phillip W.
    APPLICANT: Berman, Phillip W.
    TITLE OF INVENTION: HIV Envelope Polypeptides
    CORRESONDENCE ADDRESS:
    ADDRESSEE: MCCUtchen, Doyle, Brown & Enersen,
    STREET: 3 Embarcadero Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown & Enersen,
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81.2%; Pred. No. 1.9e-237;
ive 43; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTEK: LEAR COURGELLING
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,603A
FILING DATE: 07-UUN-1994
CLASSIFCATION 1435
PRIOR APPLICATION NUMBER: 08/072,833
FILING DATE: 07-UUN-93
ATTONENY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                         LELDKWASLWNWFDISKWLWYIK 646
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INFORMATION FOR SEQ ID NO: 30:
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IBM Compatible
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LENGTH: 857 amino acids
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Best Local Similarity 81.2'
Matches 556; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STATE: CA
COUNTRY: USA
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                                                                                                                                                                           Length 857;
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                                                                                                                                                                        85.6%; Score 2974; DB 3;
81.2%; Pred. No. 1.9e-237;
ive 43; Mismatches 46;
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REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415-393-2286
TELEFAX: 415-393-2286
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                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                    Conservative
                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 556; Conserv
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Sequence 30, Application US/09492739
Patent No. 6331404
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.

RESULT 11 US-09-492-739-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PIDDDDRNSTRNSTRVYRLISCNTSVITQACPKVSFEPIPIHFCTPAGFALLKCNNKTFNG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 IKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRVKGIRRNYQHLWRWGTWLLGILMICSAAGKLWVTVYYGVPVWKETTTTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTEVHNVWATHACVPTDPNPQEIVLENVTENFNWWKNNMVEQMHEDIISLWDQSLKPCVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNG
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                                                                                LLP
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                                                                                Епегвеп,
                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
              TITLE OF INVENTION: HIV Envelope Polypeptides NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.6%; Score 2974; DB 4; Best Local Similarity 81.2%; Pred. No. 1.9e-237; Matches 556; Conservative 43; Mismatches 46;
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                                                                                Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/492,7
FILING DATE: 27-Jan-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/134,075
                                                                              Doyle,
Center
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY, AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
Gerald R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-393-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 857 amino acids
                                                                          ADDRESSEE: McCutchen,
STREET: 3 Embarcadero
CITY: San Francisco
                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
Nakamura,
                                                                                                                                                               COUNTRY: USA
                                                                                                                                            STATE: CA
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181 VVPIEKGNISPKNNTSNNTSYGNYTLIHCNSSVITQACPKVSFEPIPIHYCTPAGFAILK 240
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                                                            61 KTEVHNVWAKHACVPTDPNPQEVLLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK 120
                                                                                                                                         121 LTPLCVTLNCTDANLNGTNVTSSSGGTMMENGEIKNCSFQVTTSRRDKTQKKYALFYKLD 180
                                                                                                                                                                                                                                                                      CNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQ 258
                                                                                                                                                                                                                                                                                                                                                     259 LKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTK 318
                                                                                                                                                                                                                                                                                                                                                                             301 LNASVQINCTRPNNNTRKSITKGPGRVIYATGQIIGDIRKAHCNLSRAQMNNTLKQVVTK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                       319 LQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNWTIGPNNTNG--T 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGIMGCSGKLICTTTVPWNASWSNKSLNMIWNNMTWMQWEREIDNYTGIIYNLLEESON 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------GAGKLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQN
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                                                                                                       LTPLCVTLHCT -- NLKNATNTKSSNWKEMDRGEIKNCSFKV----
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CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR PILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RATINGER, Hermann APPLICANT: BUCHACHER, Andrea APPLICANT: BUCHACHER, Andrea APPLICANT: BALLAIN, Claudia APPLICANT: PURTSCHER, Martin APPLICANT: TRKOLA, Alexandra APPLICANT: REGOLA, Alexandra APPLICANT: SCHMATZ, Christine APPLICANT: KLIMA, Annelies APPLICANT: KLIMA, Annelies APPLICANT: KLIMA, ANNELS APPLICANT: MUSTRY THOMAS TITLE OF INVENTION: HIV-Vaccing TILE REFERENCE: 1939-112P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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421 IKQIVNMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGSN-NSMNETFRPGGGDMRDN 479
                                                                                                                                                                                                     SGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQ 621
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                                                                480 WRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAASITLT
                                                                                                                                               540 VQARLLLSGIVQQQNNLLRAIEAQQHLLQLIVWGIKQLQARVLAVERYLRDQQLLGIWGC
                                                                                                                    503 VOARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGC
                                        WRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentil Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

84.8%; Score 2947; DB 3; Sest Local Similarity 80.1%; Pred. No. 3.4e-235; Matches 554; Conservative 40; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/07956483
Patent No. 6261799
GENERAL INFORMATION:
AFFLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND US TITLE OF INVENTION: SPECS.
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathie STREET: P.O. Box 1404
CITRET: Alexandria
STREET: Alexandria
STREEY: Alexandria
STREEY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 36,113
RELECOMMUNICATION INFORMATION:
TELEPHONE: (777)
                                                                                                                                                                                                                                                                                       622 ELLELDKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                                                                                                                                                              FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-NAY-1991
ATTONEY/AGENI INFORMATION:
NAME: CRANG-FEURY, ShAZON REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                57 AKAYDTEVHNVWATHACVPTDPNPQEIVLENVTENFNWWKNNMVEQMHEDIISLWDQSLK 116
                                                                                                                                                                                                                                                                                  58 AKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLMDQSLK 117
                                                                                                                                                                                                                                                                                                                                117 PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK----- 163
                                                                                                                                                                                                                                                                                                                                                     178 KLDIIPIDNDTTSYTLTSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 RPNNNTRKSITI--GPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFG-N 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 RPNNNTRKSIRIQRGPGRAFVTIGK-IGNMRQAHCNISRAKWNNTLKQIDSKLREQFGNN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSL 499
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                                                                                                                                                                                               1 MRVKGIRKNYQHL----WRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASD
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                                                                                                                                Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHANG, Nancy T.
APPLICANT: CALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAR & Finnegan, L.L.P.
                                                                                                                                                                39; Indels
                                                                                                                                 DB 3;
                                                                                                                                Query Match

84.6%; Score 2939.5; DB 3
Best Local Similarity 82.6%; Pred. No. 1.4e-234;
Matches 568; Conservative 34; Mismatches 39;
ORGANISM: Human imunodeficiency virus type | FBATURE: | FBATURE: | MAME/KEY: PEPTIDE | LOCATION: (79)..(184) | NAME/KEY: PEPTIDE | NAME/KEY: PEPTIDE | LOCATION: (326)..(400) | US-09-124-900-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEOELLELDKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08463210
Patent No. 6001977
GENERAL INFORMATION:
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US-08-463-210-11
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185 KLDIIPIDNDTTSYTLTSCNTSVITQACPKVSFEDIPIHYCAPAGFAILKCNNKTFNGTG 244
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82.6%; Pred. No. 1.4e-234;
ive 34; Mismatches 39; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..863
COTHER INFORMATION: /note= "env protein of HTLV-III"
US-08-463-210-11
                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

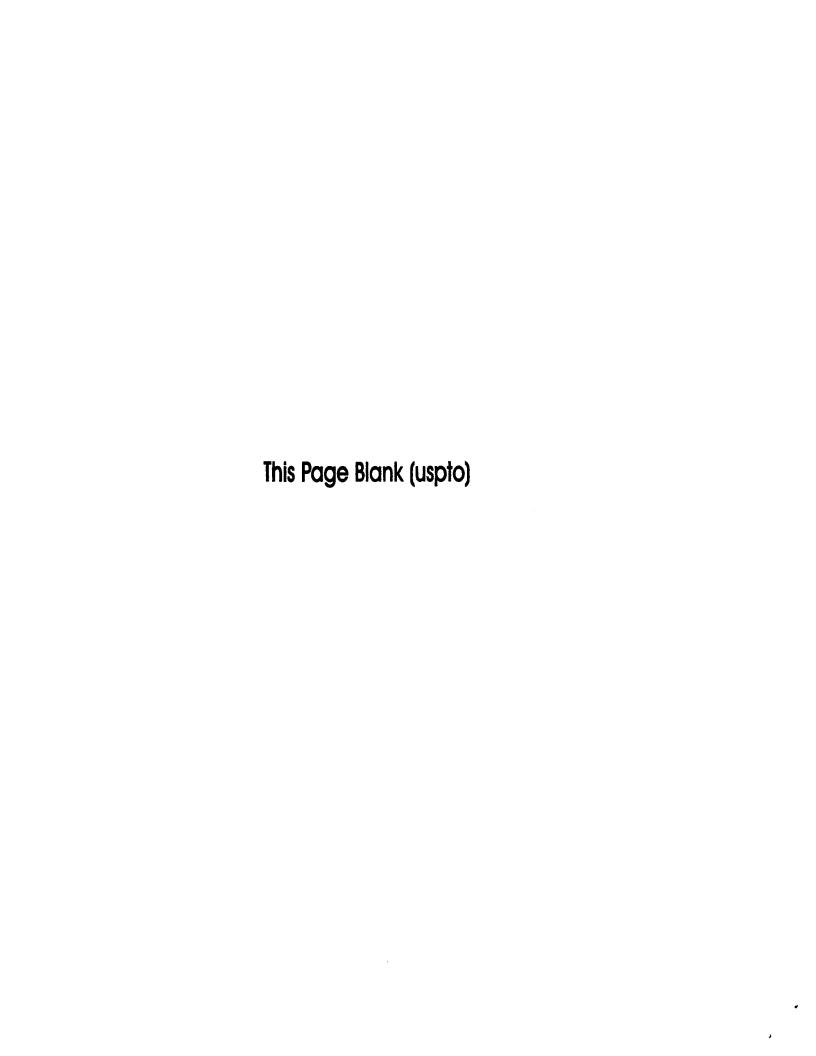
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,210

FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-OCT-1984
TTORREY, AGENT INFORMATION:
NAME: Serunian, Lealie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 863 amino acids
TYPE: amino acid
345 Park Avenue
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Matches 568; Conservative
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New York
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                                                              COUNTRY:
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NAME/KEY: Protein
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                                                                                  RDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSL 499
364 KTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTWSTNTEGSDTITL 423
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                                                                                                                                                        PCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDM
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STRAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESSES:
CORRESPONDENCE ADDRESSES:
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                      NEOELLELDKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                                                                                                                    NAME: Serunian, Leslie A.
REGISTRATION UNDRER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-0CT-1984
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08463028
Patent No. 6610476
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 751-6849
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TYPE: amino acid
STRANDEDNESS: single
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ORIGINAL SOURCE:
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US-08-463-028-11
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                                                                                                                                                                                                                                                    PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK------
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                                                                                                                                                                           Gaps
                                                                                                                                                                     47;
                                                                                                                         Length 863;
                                                                                                                      84.6%; Score 2939.5; DB 4; Length
82.6%; Pred. No. 1.4e-234;
tive 34; Mismatches 39; Indels
                                            /note= "env protein of HTLV-III'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEOELLELDKWASLWNWFDISKWLWYIK 646
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                                                                                                                                                                        Matches 568; Conservative
INAMELACATION: 1..863
COCATION: 1..863
COTHER INFORMATION: US-08-463-028-11
                                                                                                                         Query Match
Best Local Similarity
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126, App 3, Appli 3, Appli

Sequence Sequence Sequence Sequence Sequence

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Sequence Sequence

Sequence Sequence

33, Appl 6, Appli 6, Appli 6, Appli 6, Appli 147, App 3, Appli

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127, App 4, Appli 4, Appli 4, Appli 4, Appli 129, App

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Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

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Minimum Maximum Database

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PEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLANGSLAEEG 240
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Patent No. US20020127238A1
GENERAL INFORMATION:
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR FILE REFERENCE: 2570-1-002N
CURRENT APPLICATION NUMBER: 05/09/891,609
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
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US-10-003-035-33

US-10-286-332A-33

US-10-1286-915-33

US-10-190-415-6

US-10-190-435-6

US-10-190-435-6

US-10-190-435-147

US-10-190-435-126

US-10-190-435-139

US-10-190-435-149

US-10-190-435-149

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US-10-280-915-53
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TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
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                                                                    KIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIV
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| Patent No. US20020127238A1
| GENERAL INFORMATION:
| APPLICANT: Stamatactors, Leondias
| TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
| TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
| TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
| CURRENT APPLICATION NUMBER: US/09/891,609
| CURRENT PILING DATE: 2001-06-26
| PRIOR FILING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 4 O6-27
| NUMBER OF SEQ ID NOS: 4 O6-27
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                                              VVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH 300
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  FEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEG
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98.5%; Score 3422; DB 9; Length 847;
Best Local Similarity 95.4%; Pred. No. 3.1e-305;
Matches 643; Conservative 0; Mismatches 3; Indels 2
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Fatent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: HARNETT, Susan
APPLICANT: HARTIN, Exis
APPLICANT: MARTIN, Exis
TITLE OF INVENTIN, ENDI
CURRENT APPLICATION UNDBER: US/09/476,242
CURRENT PILLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
SEQ ID NO SEQ ID NOS: 26
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US-09-476-242-2
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                                                                     DIIGDIRQAHCNISGEKWNWTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
                                                   DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
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; Sequence 2, Application US/10241009
; Publication No. US20030170614A1
; GENERAL INFORMATION:
; APPLICANT: ELIM MEGSEB, Jan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; TITLE OF INVENTION NUMBER: US/10/241,009
; CURRENT FILING DATE: 2002-12-13
; CURRENT FILING DATE: 2002-12-13
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NOS: 68
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Pred. No. 3.9e-292;
2; Mismatches 7; Indels 29;
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US-10-241-009-2
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                                                                                                                                                                  YKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ 507
                                                                                                                                                                                                                                                                                                 TTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTWLIYTLIEESQNQQEKNEQELLELD 627
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Fublication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: BARNETT, SUBBAN
APPLICANT: BARNETT, SUBBAN
APPLICANT: LIAN, Ying
APPLICANT: VAN RENSBURG, Setrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILLE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190, 4355
CURRENT APPLICATION NUMBER: US/10/190, 435
SUPURARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 842
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; Sequence 2, Application US/10190305A
; Sequence 2, Application No. US20030198621A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: EARNETT. SUBJAN
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
; SOFTWARE: PATCHIIN VOY: 2.0
; SEQ ID NO 2
; LENTH: 842
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                                                                                                                                                                NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV 470
                                                                                                                                                                                    OLTVWGIKOLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM 612
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                 DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
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94.4%; Score 3279.5; DB 14; Length 842;
Best Local Similarity 94.2%; Pred. No. 3.9e-292;
Matches 619; Conservative 2; Mismatches 7; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: SF162
US-10-190-305A-2
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                          433 NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV 492
                                                                                                                                                                                                                                                                                                    493 QREKRAVTLGAMFLGFLGAAGSTWGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL 552
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LLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATG 312
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                                     DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
                                                    313 DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVWHSFNCGGE
                                                                                                                               NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV
                                                                                                             FFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
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Sequence 2, Application US/10190434B

Publication No. US20030194800A1

GENERAL INFORMATION:

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: LIAN, YING

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B

TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REPREBRICE: 2300-1621.20

CURRENT APPLICANT: 2002-07-05

CURRENT FILING DATE: 2002-07-05

NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 842
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Best Local Similarity 94.29
Matches 619; Conservative
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418 QKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKGLIRCSSNITGLLLTRDGGGE-NQTT
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                                                                                                                                                                                                                                                                                                                                                                                    VEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQ
                                                                                                                                   FGNKTIVPKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNTNGT----
                                                                                                                                                                                                                                                                                    EIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                       548 RYLKDQQLLGIMGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 -----ITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MONTAGNIER, LUC
DONJON DE SALT-MARTIN, JACQELINE
COHEN, JAQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIEESONQOEKNEOELLELDKWASLWNWPDISKWLWYIK 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 103, Application US/10026741 Publication No. US20030049604A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUILLENT, CAROLINE
GUETARD, DENISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
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 DIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGE
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                                                                          FFY CNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
                                                                                                                                                NITGLLLTRDGGKEISNTTEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVV
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Patent No. US20020155120A1

GENERAL INFORMATION:

APPLICANT: Lowell, George
APPLICANT: Lowell, George
APPLICANT: Birx, Deborah
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: 1000-21
FRIOR APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 1999-09-30
FRIOR FILING DATE: 1999-09-30
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1997-07-10
FRIOR FILING DATE: 1996-07-10
FRIOR SEQ ID NOS: 18
SOFTWARE: FastERC for Windows Version 4.0
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84.6%; Score 2937.5; DB 9.
Best Local Similarity 79.5%; Pred. No. 1.1e-260;
Matches 556; Conservative 37; Mismatches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 868
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         GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION UNMBER: US/09/476,242
CURRENT PILLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                     Score 2922.5; DB 9 Pred. No. 2.6e-259;
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81.8%;
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US20020146683A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                        861;
                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                      Indels
          NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03260.6005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Query Match

84.4%; Score 2933; DB 14;
Best Local Similarity 81.8%; Pred. No. 2.8e-260;
Matches 567; Conservative 33; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQQEKNEQELLELDKWASLWNWFDISKWLWYIK 646
                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                                                                                                                   LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
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δ 엄 Sequence 11, Application US/10196515

RESULT 11 US-10-196-515-11

Sequence 1, Application US/09476242

RESULT 10 US-09-476-242-1

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JOURNEAU INFORMATION OF THE REPENDENT HOYEL James A.

APPLICANT: LABRANCHE, Celia C.

APPLICANT: LABRANCHE, Celia C.

APPLICANT: LONG, ROBERT W.

APPLICANT: HOFFMAN, Trevor L.

TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND TITLE OF INVENTION: THERAPEUTICS

FILE REFERENCE: HOX: 9596-104U1 (0282)

CURRENT APPLICATION NUMBER: US/09/337,387

PRIOR APPLICATION NUMBER: US/09/337,387

PRIOR PALICATION NUMBER: US/09/337,387

PRIOR PLING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: US 09/317,556

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AKAYDTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AKAYETEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human immunodeficiency virus type 1 US-10-196-515-3
  656 NEQELLELDKWASLWNWFNITNWLWYIK 683
                                                                                                     Sequence 3, Application US/10196515 Publication No. US20030091594A1 GENERAL INFORMATION:
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                               APPLICANT: HOXIE, James A.
APPLICANT: HOXIE, Celia C.
APPLICANT: LABRANCHE, Celia C.
APPLICANT: LABRANCHE, Celia C.
APPLICANT: LABRANCHE, Celia C.
APPLICANT: HOME, ROBER W.
APPLICANT: HOFFWAN, Trevor L.
TITLE OF INVENTION: THERAPEUTICS
TITLE OF INVENTION: THERAPEUTICS
FILE REFERENCE: HOXIE 9596-104UI (0282)
CURRENT APPLICATION NUMBER: US/10/196,515
CURRENT APPLICATION NUMBER: US/09/337,387
PRIOR APPLICATION NUMBER: US/09/337,387
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/317,556
PRIOR APPLICATION NUMBER: US 09/317,556
SPRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENT NOS: 12
SEQ ID NO 11
LENGTH: 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AKAYDTEVHNVWATHACVPIDPNPQEVLVNVTENFDWRKNDMVEQMHEDIISLWDQSLK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK----- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPNNNTRKSITI--GPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFG-N 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSVNFTDNAKTIIVQLNTSVEINCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.7%; Score 2907.5; DB 1/81.7%; Pred. No. 6.2e-258;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 562; Conservative
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180 PIPIHYCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEBEVV 239
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                              TW-NNTIGPNNTNG-TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
RSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLGAAGSTMGAASMALTV
                                                                                                                                                                                                                                                                                                                 APPLICANT: BILLEY, JAMES M
APPLICANT: SCHUELKE, NORBERT
APPLICANT: SCHUELKE, NORBERT
APPLICANT: OLSON, WILLIAM C
APPLICANT: OLSON, WILLIAM C
APPLICANT: JOHN, MOORE P
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
FILE REPERENCE: 2046/25931az
CURRENT APPLICATION NUMBER: US/10/032,162
FRICE REPLICATION NUMBER: US/10/032,162
FRICE REPLICATION NUMBER: 05/602,864
FRICE FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDFNPQEVVLENVT
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                                                                                           GKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQE
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Pred. No. 6.2e-254;
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                                                                                                                                                                                       LLELDKWASLWNWFIISSWLWYIK 678
                                                                                                                                                            LLELDKWASLWNWFDISKWLWYIK
                                                                                                                                                                                                                                                                      ; Sequence 13, Application US/10032162; Publication No. US20030052839A1
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al Similarity 84.5%;
545; Conservative 25
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                | FUBLICANT: LADRANTION:
| GENERAL INFORMATION:
| APPLICANT: HOXIE, James A.
| APPLICANT: LABRANCHE, Celia C.
| APPLICANT: LABRANCHE, Celia C.
| APPLICANT: LOMS, Robert W.
| APPLICANT: LOMS, Robert W.
| TITLE OF INVENTION: COL: INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND TITLE OF INVENTION: THERAPEUTICS.
| TITLE OF INVENTION: UNBER: US/10/196,515 |
| CURRENT APPLICATION NUMBER: US/09/337,387 |
| PRIOR FILING DATE: 1999-06-22 |
| PRIOR FILING DATE: 1999-06-24 |
| NUMBER OF SEQ ID NOS: 12 |
| SEQ ID NO 12 |
| SEQ ID NO 12 |
| LENGTH: 759 |
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Best Local Similarity 81.1%; Pred. No. 1.1e-255;
Matches 555; Conservative 38; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Human immunodeficiency virus type 1
US-10-196-515-12
                                                               LLELDKWASLWNWFDISKWLWYIK 646
                                                                              LIELDKWASLWNWFNITNWLWYIK 678
                                                                                                                                                                            Sequence 12, Application US/10196515
Publication No. US20030091594A1
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382 YKYKVVKIEPLGVAPTKCKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARL 441
                                      LLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLI
                                                                                                                                 442 LLSGIVQQQNNLLRAIEAQQRMLQLTVWGIKQLQARVLAVERYLGDQQLLGIWGCSGKLI
                                                                                                              CTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLEL
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Publication No. US20030052839A1

GENERAL INFORMATION:

APPLICANT: BINLEY, JAMES M

APPLICANT: OLSON, WILLIAM C

APPLICANT: PAUL, MADDON WILLIAM C

APPLICANT: PAUL, MADDON STABLIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF

TITLE OF INVENTION STABLIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF

FILE OF INVENTION NUMBER: US/10/032,162

CURRENT APPLICATION NUMBER: US/10/032,162

CURRENT FILING DATE: 2000-10-24

PRIOR PELING DATE: 2000-6-23

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 15

LENGTH: 579

WANDEL TO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 ------GAG----CDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNGKGP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 FNHSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTEGSNNTEGNTITLPCRIKQII 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 PNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIV 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 NRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWWQEVGKAMYAPPIRGQIRCSSNITGLLLIRDGGIN-ENGTEIFRPGGGDMRDNWRSEL 381
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                                                      540 QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREID
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                                    481 AMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 GEIKNCSFKVGAGKLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGP
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                                                                                                                                                                                    600 NYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWY 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.8%; Score 2771; DB 14;
Best Local Similarity 85.6%; Pred. No. 1.2e-245;
Matches 529; Conservative 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-032-162-15
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US-10-032-162-15
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

February 25, 2004, 14:12:55; Search time 18.3842 Seconds (without alignments) 3380.063 Million cell updates/sec Run on:

US-09-891-609A-2

Perfect score:

3474 1 MRVKGIRKNYQHLWRGGTLL.....DKWASLWNWFDISKWLWYIK 646 Sequence:

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

envelope glycoprot
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| gag polyprotein - | env protein - huma | envelope polyprote | env polyprotein - | envelope polyprote | envelope polyprote | envelope polyprote | envelope polyprote | env polyprotein pr | env polyprotein pr | envelope polyprote | envelope polyprote |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A53034            | S25940             | 860538             | 860528             | S60545             | S60524             | S60529             | C46356            | S60548             | S60546             | S60547             | S60521             | VCLJGG             | VCLJST             | 860532             | 860531             |
| 7                 | 7                  | 7                  | 0                  | 7                  | N                  | 0                  | 7                 | 7                  | 7                  | 7                  | 0                  | -                  | П                  | 7                  | 7                  |
| 863               | 290                | 297                | 299                | 294                | 294                | 299                | 877               | 301                | 300                | 300                | 299                | 852                | 859                | 301                | 301                |
| 50.4              | 37.4               | 37.0               | 34.2               | 34.2               | 34.2               | 34.1               | 34.1              | 33.9               | 33.8               | 33.7               | 33.6               | 33.6               | 33.6               | 33.5               | 33.5               |
| 0.5               | 1301               | 1286               | 1189               | 1188.5             | 1187.5             | 1186               | 1183              | 1179               | 1173.5             | 1169.5             | 1169               | 1167.5             | 1166               | 1163               | 1163               |
| 175               |                    |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

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392 EVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYK 451

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cipecies: human immunodeficiency virus type 1 (strain sc14.3)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Sate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12016
A;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in States preliminary; branslated from GB/EMBL/DDBJ
A;Reference number: Z17379; MUID:98178116; PMID:9519894
A;Reference number: Z17379; MUID:98178716; PMID:9517894
A;Reference number: Z17379; MUID:98178716; PMID:951787111; PID:92351784
A;Reference number: Z17379; PMID:971783; PIDN:AACS9271.1; PID:92351784
A;Reference number: Z17379; PMID:971783; PIDN:AACS9271.1; PID:92351784
C;Guperfamily: type E retrovirus env polyprotein
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                          GGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNWTIGPNNTNGTITLPCRIKQIINRWQEVG
                                                                                                                                                                                                         KAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVK
                                                                                                                                                                                                                                                                                                          I EPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                515 QONNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPW
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87.1%; Score 3025.5; DB 2; Length
Best Local Similarity 84.3%; Pred. No. 8.4e-211;
Matches 575; Conservative 34; Mismatches 34; Indels
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658 NWFDITKWLWYIK 670
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H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N/Alternate names: coat polyprotein
N/Alternate names: coat polyprotein
N/Alternate names: coat protein gp12): coat protein gp11.
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: al-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C;Accession: H44001
S;Li, Y; Hui, H; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J, Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties 0.
A;Residues: A44001; MUID: 93021387; PMID: 1404605
A;Residues: L-843 <-LIX-
A;Residues: L-843 <-LIX-
A;Coss references: GB:M93258
C;Genetics:
A;Gene: env
C;Superfamiy: type E retrovirus env polyprotein; transmembrane protein
C;Superfamiy: type E retrovirus env polyprotein; transmembrane protein
C;Superfamiy: signal sequence #status predicted <-GPI>F;19-35/Region: hydrophobic
F;19-35/Region: hydrophobic
F;30-843/Product: coat protein gp12 #status predicted <-GPI>F;499-515/Region: hydrophobic
F;738-755/Domain: transmembrane #status predicted <-TWN>F;738-755/Domain: transmembrane #status predicted <-TWN>F;738-755/Domain: transmembrane #status predicted <-TWN>F;737,251,287,237,251,297,237,251,297,327,351,381,389,395,400,435
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                                                                                                                                                         570
                                                        511
                                                                                                        538
                                                                                                                                                                                    VPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWA 630
                                                                                                                                                                                                                                                                                          599 VPWNASWSKLDRIWNMTWMEWEREIDNYTSEIYTLIEESQNQQEKNEQELLELDKWA 658
     EVGKAMYAPPIRGOIRCSSNITGLLLTRDGGIN-ENGTEIFRPGGGDMRDNWRSELYKYK 478
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                                                        VVKI EPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSG
                                                                                   IVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTA
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87.3%; Score 3012; DB 1; Length 84;
Best Local Similarity 84.2%; Pred. No. 2.8e-211;
Matches 567; Conservative 38; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             SLWNWFDITKWLWYIK 674
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| a 8                                     | 301 NTRKSIHIGPGQALYATGAIGDIRQAHCNISRAKWNNTLKQIVKKLKVQFGNKTIIFNQ 360   | 360 SGGDPEIVMHSFNCGGEFFYCNSTQLANSTWANNTEGSNATEGNTITLPCRIKQPINAWQ   |
|---|---|--|
| 5 A                                     | SSGGDPEIVMHSFNCGGEFFYCNTTKLFNSTWMFNNTWNDTEDTEGNGTITLFCRIKQ 41   | Db 420 EVGKAMYAPPIRGQIRCSSNITGLIFTRDGGALSNITELFREGGGDMRDNWRSELYKYK 478   |
| දු දු                                   | 386 IINRWQEVGKAMYAPPIRGOIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRS 445  | Qy 452 UVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSG 511  |
| <u>ک</u> ۾                              | 446 ELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQA 505  | QY 512 IVQQQNNLLRAIBAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTA 570<br>  |
| <b>상</b> 됨                              | 506 RQLLSGIVQQNNLLRAIBAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGK 564   | QY 571 VPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWA 630  |
| දු පු                                   | 565 LICTTAVPWNASWSNKSLDQIWNNATWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELL 624  | Oy 631 SLWNWPDISKWLWYIK 646<br>  |
| රු සි                                   | 625 ELDKWASLWNWFDISKWLWYIK 646  | RESULT 5 VCLJA2  |
| RESUL1<br>S13289                        | 4   | env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2) N.Alternate names: coat polyprotein C.Species: human immunodeficiency virus type 1, HIV-1 A.Note: host Homo sapiens (man)  |
| env pi<br>C;Spec<br>C;Date              | otein - human immunodeficiency virus type 1<br>ies: human immunodeficiency virus type 1, HIV-1<br>: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997                                       | C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999 C; Accession: A03976 R; Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi   |
| C; Acce<br>R; O'B1<br>Nature<br>A: Titl | BB10n: \$13289<br>ien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A<br>348, 69-73, 1990<br>e: HIV-1 tropism for monomuclear phacocytes can be determined by regions of cm120 | Science 227, 484-492, 1985 A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2). A;Reference unuber: A04003; MUID:85090453; PMID:2578227 A;Accession: A01976   |
| A; Refe<br>A; Acce<br>A; Stat           |   | A;Molecule type: DNA<br>A;Residues: 1-855 <san><br/>A;Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666</san>   |
| A; Resi<br>C; Supe                      | dues: 1-847 <08R><br>rfamily: type E retrovirus env polyprotein   | A Genericans C; Superfamily: type E retrovirus env polyprotein   |
| Que:<br>Best<br>Matc                    | Query Match  86.6%; Score 3008; DB 2; Length 847;  Best Local Similarity 84.6%; Pred. No. 1.5e-209;  Matches 572; Conservative 29; Mismatches 43; Indels 32; Gaps 6;  | Cyncywords: Albs; capsid procesn; coat procesn; glycoprocesn; immunouesiciency; polyproce<br>F;1-30/Domain: signal sequence #status predicted <505<br>F;31-509/Product: exterior membrane glycoprotein #status predicted <ext><br/>F;510-855/Product: transmembrane glycoprotein #status predicted <twm></twm></ext> |
| රි සි                                   | MRVKGIRKNYQHLMRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY  | F;87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458, F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted  |
| 3 &                                     | 1 DIEVENVÄATHACVPTDPNPQEIVLENVTENFNMMKONNNVEQMEDIISLMPQSLKPCVK 120  | Query March<br>Best Local Similarity 82.4%; Pred. No. 8.5e-208;<br>Matches 563; Conservative 34; Mismatches 48; Indels 38; Gaps 6;   |
| ብ <i>እ</i>                              | 61 DIEVHNVWATHACVPTDBNPQEVVLENVTENFNMWKNNMVEQMQEDIISLMDQSLKBCVK 120 121 LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG  | QY 1 MRYKGIRKNYQHLMRGGTLLIGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY 60  :     :     :  |
| д                                       |   | OY 61 DTEVHNVWATHACVPTDPNPQEIVLENVTENPNWANNWVEQMHEDIISLWDQSLKPCVX 120  |
| රු සි                                   | 163KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNV 213  | Db 61 DTEVHNVWATHACVPTDPNPQEVVLGNVTENFNMWKNNMVEQMQEDIISLWDQSLKPCVK 120 Qy 121 LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG162  |
| à i                                     | STVQCTHGIRPUVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNN  |  |
| යි සි                                   | 240 STVDCTHGIRPVVSTQLLLNGSLABEBEVVIRSDNFTNNAKTIIVQLKESVEINCTRPNNN 299<br>274 TRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQS 333   | Oy 163   |
| 음 <i>장</i>                              | 300 TRKSIHIGPGRAFYTTGEIIGDIRQAHCNISRAKWNDTLKQIVIKURRQFENKTIVFNHS 359<br>334 SGGDPEIVWHSFNCGGEFFYCNSTQLFNSTW-NNTIGPNNTNG-IITLPCRIKQIINRWQ 391  | Qy 209 PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCT 268  |

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al Similarity 82.6%; Pred. No. 1.4e-204;
568; Conservative 34; Mismatches 39;
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                                                                                      -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPC
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Nylternate names: coat polyprotein
Nylternate names: coat polyprotein
Nylternate names: coat polyprotein
Nylontains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: A31667
C;Accession: A31667
N;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S
Virology 168, 79-89, 13089
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-A;Reference number: A94389; MUD:89085613; PMID:2789516
A;Moccule type: DNA
A;Residues: 1-852 cANA>
C;Superfamily: type E retrovirus env polyprotein; transmembrane protein
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F;1-516/Product: coat protein gp120 #status predicted <CP2>
F;517-852/Product: coat protein gp41 #status predicted <CP2>
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PCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCT
                                                                                                                                                                                                                                                                                                                         KTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNN----TIGPNNTNG--TITL
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                                                                  ---LINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSG
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C;Species: human immunodeficiency virus type 1.
C;Species: human immunodeficiency virus type 1. HIV-1
C;Species: human immunodeficiency virus type 1. HIV-1
C;Species: human-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33985
B;Carlini, F.
Submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Accession: S33985
A;Accession: S33985
A;Residues: 1-881 <CARA
A;Residues: 1-881 <CARA
A;Residues: 1-881 <CARA
A;Residues: L981 <CA
                                                                                                                                                                                                                                                                                                                                         298 EINCTRPNNNTRKSIRIQRGPGRAFVTIGK-IGNWRQAHCNISRAKWNATLKQIASKLRE
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82.5%; Pred. No. 9.5e-204;
ive 34; Mismatches 42;
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564; Conservative
      567; Conservative
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N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Bate: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Main-Hobson, S: Sonigo, P: Danos, O: Cole, S: Alizon, M.
Call 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Residues: 1-861 <WAI>
A;Censeios: A03975
A;Molecule type: DNA
A;Residues: Centernate and DNA
A;Censeios
C;Genetics:
C;G
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                                        DIEAHNVWATHACVPTNPNPQEVVLENVTENFNWMKNNWVEQMHEDIISLWDGSLKPCVK 122
                                                                                                                                                            KFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKES 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQ 322
      DTEVHNVWATHACVPTDPNPOEIVLENVTENFNMWKNNMVEQMHEDIISLWDOSLKPCVK 120
                                                                                                                                                                                                                                                                                   -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDK
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                                                                                                                             LTPLCVTLHCT--NLKNATNTKSSN----WKEMDRGEIKNCSFKVGAG-------
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Pred. No. 4.2e-204;
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C.Species: human immunodeficiency virus type 1
C.Species: human immunodeficiency virus type 1, HIV-1
C.Date: 19-Mar-1997 #text_change 31-Oct-1997
C.Accession: S13288
R.O Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, J.A
Nuture 348, 69-73, 1990
A.Filte: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20 of A.Reference number: S13288 MUID:91043044; PMID:2172833
A.Reference number: S13288
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-854 cOBR>
C.Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                          58 AKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLK 117
                                                                                                                    1 MRVK---EKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTVYYGVPVWKEATTTLFCASD
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                                                                                            1 MRVKGIRKNYQHL----WRGGTLLLGMLMICSAVBKLWVTVYYGVPVWKEATTTLFCASD
                                                                                                                                                                                                                                                                               PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK-----
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  Query Match 84.2%; Score 2926.5; DB 1. Best Local Similarity 82.1%; Pred. No. 1.2e-203; Matches 565; Conservative 35; Mismatches 41;
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C. Species: human immunodeficiency virus type 1, HIV-1
A. Mote: host Homo sapiens (man)
C. Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C. Accession: A03974
R. Mature 313, 450-458, 1985
A. Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retroving Reference number: A93355, MUID: 85111157; PMID: 2982104
A. Reference number: A93355, MUID: 85111157; PMID: 2982104
A. Residues: 1-856 «MUE»
A. Residues: 1-856 (Rue)
A. Residues: 1-856 (Ru
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MRVK---EKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTVYYGVPVWKEATTTLFCASD
                                               AKAYDTEVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLK
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MRVKGIRKNYOHLWR----GGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASD
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NiAlternate names: coat polyprotein
NiAlternate names: coat polyprotein
NiAlternate names: coat polyprotein
NiAlternate names: coat protein gp120; coat protein gp32
CiSpecies: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996
C;Accesion: 842995
R;Shimizu, H; Hasebe, F; Tsuchie, H; Morikawa, S; Ushijima, H; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analygis of a human immunodeficiency virus type 1 isolate carrying a truncated A;Reference number: A42995; MUID:92351552; PMID:1322587
A;Accesion: B42995
A;Molecule type: mRNA
A;Residues: 1-729 cSHI>
A;Cross-references: GB:S41266; GB:D01206
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein; transmembrane protein
E;1-689/Domain: extracellular #status predicted cSIG>
F;1-33/Domain: signal \*status predicted cSIG>
F;1-33/Domain: status predicted cSIG>
F;1-35/ env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

F;17-33/Region: hydrophobic #status predicted

F;34-517/Region: cleavage processing #status predicted <CPl>
F;514-517/Region: cleavage processing #status predicted
F;518-729/Product: coat protein gp32 #status predicted <CP2>
F;518-729/Region: hydrophobic #status predicted
F;518-534/Region: hydrophobic #status predicted <TM1>
F;690-711/Domain: transmembrane #status predicted <TM1>
F;712-729/Domain: intracellular #status predicted <INT>
F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414, æ 534 114 120 203 239 263 299 323 359 376 414 432 474 492 551 594 611 654 9 54 415 ITLPCRIKQIVNMMQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGNTQNNNTNSSIBIF SDAKAYDTEVHNVWATHACVPTDENPQEIVLENVTENFNWWKNNWVEQMHEDIISLWDQS 61 SDAKAYDTEAHNVWATHACVPTDPNPQEVVLVNVTENFNWWKNNWVEQMHENIISLWDQS -----KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKK PNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESV 240 FNGTGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEBGVVIRSENFTDNVKTIIVQLNETV 264 EINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQF 324 GNKTIVFKOSSGGDPEIVMHSFNCGGEFFYCNSTQLFNST------WNNTIGPNNTNGT 360 ENKTIVFNQSSGGDPEIVWHNFNCGGEFFYCDSSQLFNSTHLSNGTWWNGT-GPEN----377 ITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTT----EIF 433 RPGGGDMRDNWRSELYKYKVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGS TWGARSLILTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLK TMGAAAVTLTVQARQLLPGIVQQQNNLLRAIDAQQHLLQLTVWGIKQLQARVLAVERYLK DOQLIGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEE 1 MRVKGIRKNYQHLW-----RGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCA LKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEMDRGE1KNCSFKVGAG-------55; DB 1; Length 729; Indels 49; 646 689 83.7%; Score 2908.5; DB 79.0%; Pred. No. 2e-202; iive 42; Mismatches 4 SONOGEKNEGELLELDKWASLWNWFDISKWLWYIK SONOGEKNEQDILLALDKWDSLWNWFSITKWLWYIK Local Similarity 79.0 nes 549; Conservative Query Match Best Local S: Matches 549 493 552 655 535 55 115 612 163 204 셤 g 셤 ઠે 8

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RESULT

NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
NyContains: coat protein gp120; coat protein gp41
NyContains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: name immunodeficiency virus type 1, HIV-1
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 01-Mar-1996
C;Accession: A42995
R;Shimizu, H; Hasebe, F; Tsuchie, H; Morikawa, S; Ushijima, H; Kitamura, T.
Nirology 189, S34-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t

Search completed: Pebruary 25, 2004, 14:19:20 Job time : 20.3842 secs

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A; Reference number: A42995; MUID:92351552; PMID:1322587
A; Accession: A42995
A; Molecule type: mRNA
A; Residues: 1-661 <SHI>
A; Cross-references: GB:S41266; GB:D01206
C; Genetics:
A; Gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG------- 162
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protein search, using sw model OM protein Pebruary 25, 2004, 14:03:35 ; Search time 11.2348 Seconds
(without alignments)
2994.034 Million cell updates/sec Run on:

US-09-891-609A-2 3474 Title: . Perfect score:

1 MRVKGIRKNYQHLWRGGTLL......DKWASLWNWPDISKWLWYIK 646 Sequence:

**BLOSUM62** Scoring table: 141681 segs, 52070155 residues Searched:

Gapop 10.0 , Gapext 0.5

Potal number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | P19550 human immun |           | P20871 human immun | P05878 human immun | 378       | P04579 human immun | P12488 human immun | 375    | n        | P12489 human immun | P03377 human immun | P20888 human immun |           | P04578 human immun | P04582 human immun | P19549 human immun | P31819 human immun | P05877 human immun | P04624 human immun | P31872 human immun | Q70626 human immun | P05880 human immun | P19551 human immun | 882 human | 0458      | 28        | 18        | P05881 human immun | P18799 human immun | 31        | 72   | 0         | P12491 human immun |
|-----------|---------------|--------------------|-----------|--------------------|--------------------|-----------|--------------------|--------------------|--------|----------|--------------------|--------------------|--------------------|-----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|-----------|-----------|-----------|--------------------|--------------------|-----------|------|-----------|--------------------|
| SUMMARIES | ID            | ENV HV1S1          | ENV_HV1Y2 | ENV_HV1JR          | ENV_HV1SC          | ENV_HV1A2 | ENV_HV1RH          | ENV_HV1BN          |        |          | ENV_HV1J3          | ENV_HV1BR          | ENV_HV10Y          | ENV_HV1PV | ENV HV1H2          | ENV_HV1B8          | ENV_HV1S3          | ENV_HV1KB          | ENV_HV1MN          |                    |                    |                    |                    | ENV_HV1MF          | ENV_HV1Z8 | ENV_HV1MA | ENV_HV1Z6 | ENV_HV1Z2 | ENV HV1ZH          | ENV_HV1ND          | ENV_HV1EL |      | ENV_HV1NS | ENV_HV1Z3          |
|           | DB            | 1                  | н         | ٦                  |                    | Н         | -                  | ٦                  | Н      | <b>-</b> | -                  | -                  | -                  | ч         | -                  |                    | Н                  | -                  | -                  |                    | -                  | н                  | П                  |                    | -         | -         | -         | 7         | 7                  | -                  | Н         | Н    | н         | ٦                  |
|           | Length        | 47                 | 4         | 4                  | വ                  | n         | 9                  | വ                  | LO.    | 9        | ø                  | ø                  | ß                  | n         | n                  | ഹ                  | ហ                  | 9                  | n                  | ഹ                  | ഹ                  | 826                | 4                  | വ                  | 9         | ഹ         | ഹ         | വ         | ഹ                  | 4                  | £         | 854  | 421       | 460                |
| مد        | Query         | 00                 | 87.3      | 9                  | 86.3               | S         | 84.8               | 84.7               | 84.6   | 84.6     | 84.5               |                    |                    | 84.2      |                    |                    | 83.9               | ë.                 | ۳,                 | ۳.                 | m                  | 83.2               | m                  | щ.                 |           | 77.1      | 76.9      | ė.        | 75.8               |                    | ٠         |      | 49.3      |                    |
|           | Score         | 3422               | 3032      | 3002.5             | 2997.5             | 2984      | 2947               | 2941.5             | 2939.5 | σ        | 2935               | 2933               | 2929               | 2926.5    | σ                  | 2918               | 2913.5             | o                  | 2904               | œ                  | 2894.5             | 2891.5             |                    | 2885.5             |           | 2678.5    | 2672      |           | 2632.5             | Φ                  | 2595      | 2196 | 1713.5    | 1649.5             |
|           | Result<br>No. | п                  | 7         | m                  | 4                  | 2         | 9                  | 7                  | 80     | σ        | 10                 | 11                 | 12                 | 13        | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 50                 | 21                 | 22                 | 23                 | 24        | 25        | 56        | 27        | 28                 | 29                 | 30        | 31   | 32        | 33                 |

| Q02837 simian immu |           |           |           |           |           |           |           |           |           |           |           |
|--------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| ENV_SIVAI          | ENV_SIVAG | ENV_HV2G1 | ENV_SIVA1 | ENV_HV2ST | ENV HV2S2 | ENV_HV2CA | ENV_SIVAT | ENV_HV2D1 | ENV HV2BE | ENV HV2NZ | ENV_SIVMK |
| н,                 | ٠,        | -         | 7         | -         | -         | -         | -         | -         | -         | -         | -         |
| 854                | 877       | 851       | 768       | 859       | 712       | 859       | 865       | 851       | 860       | 856       | 881       |
| 35.0               | 34.1      | 33.6      | 33.6      | 33.5      | 33.1      | 33.1      | 32.7      | 32.6      | 32.6      | 32.5      | 32.3      |
| 1215.5             | 1183      | 1167.5    | 1166      | 1165      | 1151      | 1149.5    | 1136.5    | 1131.5    | 1131      | 1130.5    | 1120.5    |
| 34                 | 3.5       | 36        | 37        | 38        | 39        | 40        | 41        | 42        | 43        | 44        | 45        |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M65024; AAA45072.1; -.
PDB; 10BE; 15-MXY-97.
HIV; M38428; ENVSFICE;
InterPro; IPR000328; Env GP41.
InterPro; IPR00777; GP120.
Pfam; PF00515; GP120, 1.
Pfam; PF00517; GP11; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                           Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
"Viral determinants of human immunodeficiency virus type 1 T-cell or
"viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398(1990).
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                                                                                                                                                                                                             Human immunodeficiency virus type 1 (SP162 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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BY SIMILARITY.
CHOUSE (GLCNAC. ...) (POTER N-LINKED (GLCNAC. ...)) (POTER N-LINKED (GLCNAC. ...) (POTER N-LINKED (GLCNAC. ...)) (POTER N-LINKED (GLCNAC. ...) 
                                                                                                                     01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior
                                                                                                                                                                                      glycoprotein (GP120); Transmembrane glycoprotein (GP41)]
                                                   847 AA.
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=90347835; PubMed=2384920;
                                                                                              01-FEB-1991 (Rel. 17, Created)
                                                   STANDARD;
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P19550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG--------
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               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                        Length 847;
                                                                                                                                                                                                                                                                                          0A901317FD7FF2AB CRC64;
                                                                                                                                                                                                                                                                                                                       Score 3422; DB 1;
Pred. No. 1.5e-256;
0; Mismatches 3;
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al Similarity 95.4%;
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PIR; H44001; H44001.

PDB; 1G9N; 27-DEC-00.

InterPro; IPR000328; PR GP41.

InterPro; IPR00077; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; S1GNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";
                                 01-07N-1994 (Rel. 29, Created)
01-07N-1994 (Rel. 29, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
Shaw G.M.;
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                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses, Retroid viruses; Retroviridae, Lentivirus.
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=36377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRVKGIRKNYQHLWRGGTLLLGMLM1CSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                              AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL N-LINKED (GLCNAC. ...
                     (HIV-1)
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                  Human immunodeficiency virus type 1 (JRCSF isolate)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 86.4%; Score 3002.5; DB 1; il Similarity 83.9%; Pred. No. 4e-224; 568; Conservative 31; Mismatches 45;
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                                                                         SEQUENCE FROM N.A.

Koyanagi S., Chen I.S.Y.;

Submitted (DEC-1988) to the HIV data bank.
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HIV; M38429; ENV$RCSF.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP121: 1.
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01-FBB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                                                                                 Score 3032; DB 1;
Pred. No. 2.1e-226;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                          Pfem; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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InterPro; IPR000777; GP120.
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Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1989).
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
51yelope polyprotein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGBI_TaxID=11702;
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MEDLINE=85090453; PubMed=2578227;
Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
Sanchez-Pescador R., Power M.D., Gee W.W., Renard A., Randolph A.,
Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
Levy J.A., Dina D., Luciw P.A.;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein (BP160 precursor [Contains: Exterior glycoprotein (GP160); Transmembrane glycoprotein (GP120);
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Science 227:484-492(1985).
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PIR; A03976; VCLJA2.

HIV; K02007; ENV$SF2.

InterPro; IPR0000328; Env GP41.

InterPro; IPR00077; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

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                                                                                                                                                                                                                                         GLYCOPROTEIN
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EXTERIOR MEMBRANE GLYCOPROTEIN
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BY SIMILARITY.
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EXTERIOR MEMBRANE GLYCOPROTEIN
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                 GLYCOPROTEIN
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Pred. No. 8.1e-220;
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             TRANSMEMBRANE G
BY SIMILARITY.
N-LINKED (GLCNAN).
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80.1%;
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554; Conservative
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865 AA;
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                                                                                   IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGPNNTNGTITLPCRIKQ 385
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                  RPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFG-NKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86218077; PubMed=2423250;
ASTACTICH B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
"Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M17451; AAA45057.1; -.
HIV; M17451; ENVSRF.
InterPro; IPR0001328; ENV GP41.
InterPro; IPR000137 GD120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865
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P04579:
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ENV_HV1RH
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| Oy         319         LOAOFGNKTIVFKOSSGGDPEIVMHSFNCGGEFFYCNSTOLFNSTWNNTIGPNNTNGT         376           1  | V_HV1BN PENV_HV1BN PINABN PLA488; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 10-OCT-1989 (Rel. 12, Last sequence update) 10-OCT-2003 (Rel. 12, Last sequence update) 11-OCT-2003 (Rel. 12, Last sequence update) 12-OCT-2003 (Rel. 12, Last sequence update) 13-OCT-2003 (Rel. 12, Last sequence update) 1 | RT "Blological and molecular characterization of human immunodeficiency RT virus (HIV-IBR) from the brain of a patient with progressive RT virus (HIV-IBR) from the brain of a patient with progressive RT dementia.";  RL Virology 168.79-89(1989).  CC |   |

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KTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTKGSNNTEGSDTITL 416
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 NMWQEVGKAMYAPPIRGQIKCSSNITGLLLTRDGGNNNETTDTEIFRPGGGNMRDNWRSE 478
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                                   LYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQAR
                                                      ICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLE
                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP41)].
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"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gpl20) expressed in Chinese hamster ovary cells.";
J. Blol. Chem. 265:10373-10382(1990).
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MEDLINE-8111123; PubMed=2578615;
MEDLINE-8111123; PubMed=2578615;
Josephs S. F., Bozan E. R., Rafalski J.A., Whitehorn E.A.,
Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
Wong-Staal F.,
"Complete nucleotide gequence of the AIDS virus, HTLV-III.";
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MEDLINE-90285159; PubMed-2355006;
Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
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HIV; MIS654; ENVSHH102.
InterPro; IPR0001328; Env GP41.
InterPro; IPR0001328; Env GP41.
Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP41; 1.
Pfam; PR01517; GP41; 1.
AIDS; Cat protein; Polyprotein; Gl Signal.
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Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
DeVico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarngadharan M.G.;
"Characterization of the secreted, native gpl20 and gpl60 of the human immunodeficiency virus type 1.",
AIDS Res. Hum. Retroviruses 6:371-380(1990).
                                                               RDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLGAAGSTMGAASM
                                                                                                                                       WGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEK
          PCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDM
                                                  RDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSL
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane 91ycoprotein (GP120); Transmembrane 91ycoprotein (GP41)].
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MEDLINE=87041461; PubMed=3490666;
MEDLINE=87041461; Debace S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
Andersen P.R., Devare S.G.;
"Molecular cloning and primary nucleotide sequence analysis of a
distinct human immunodeficiency virus isolate reveal significant
                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986)
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PIR; C25523; VCLJH4.
HIV; M13137; ENV$CDC45.
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HIV; M21138; ENVSJH3.
InterPro; 1PR000328; Env GP41.
InterPro; IPR000316; GP120; 1.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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01-0CT-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior of glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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MEDLINE=89352108; PubMed=2669897;
Komiyama N., Hattori N., Inoue J., Sakuma S., Involeotide sequences of gag and env genes of "Nucleotide sequences of any bacteria.";
AIDS Res. Hum. Retroviruses 5:411-419(1989).
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                                                                                                                                                                                                                                                                                                                     MEDLINE=90148544; PubMed=2559749;
Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.
Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.
Hughly defective HV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
AIDS 3:707-715(1989).
-!- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
                                                                                                                             01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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TRANSMEMBRANE GLYCOPROTEIN.
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INCETPRO; IPR000328; ENV GP41.
INCETPRO; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (OYI isolate) (HIV-1) Viruses; Retroid viruses; Retroviridae; Lentivirus. VCBI_TaxID=11699;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL N-LINKED) (GLCNAC. ...)
                                                                                                                                                                                                                                                     EMBL; K02083; AAB59873.1; -.
EMBL; X01162; CAA25903.1; ALT_SEQ.
PIR; A03974; VCLJVU.
InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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                                                                                         "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus."; Nature 313:450-458(1985).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11700;
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                                    SEQUENCE FROM N.A.
MEDLINE=85111157; PubMed=2982104;
Muesing M.A., Smith D.H., Cabradilla C.D.,
Capon D.J.;
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58 AKAYDTEVHINVWATHACVPTDPNPQEVVLVNVTENFNWWKNDWVEQWHEDIISLWDQSLK 117
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                                                                                                       1 MRVKGIRKNYQHL----WRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASD
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19.4579; 13.40719; 13.40719; 13.4071999 (Rel. 05, Created)
15.401.1999 (Rel. 38, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP120)].
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MEDLINE=87299196; PubMed=3040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Stal F.;
"Complete nucleotide sequences of functional clones of the AIDS
                                                      47;
                                                                                                                                                                                                                                                                                                                117 PCVKLTPLCVTLHCTNLKNATNTKSSNWKE-MDRGEIKNCSFKVGA---GK-
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Viruses11706;
  Length
                                                   41; Indels
Query Match

84.2%; Score 2926.5; DB 1;
Best Local Similarity 82.1%; Pred. No. 3.1e-218;
Matches 565; Conservative 35; Mismatches 41;
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298 RPNNNTRKRIRIQRGPGRAFVTIGK-IGNMRQAHCNISRAKWNNTLKQIASKLREQFGNN 356
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                (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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                                                                                                  DB 1; Length 856;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11684;
[1]
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ENV HV1B8

STANDARD; PRT; 851 AA.

AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein (9160 precursor [Contains: Exterior DE Glycoprotein (GP10); Transmembrane glycoprotein (GP41)].

GN ENV.
                                                                                                Query Match 84.1%; Score 2922.5; DB 1; Length Best Local Similarity 81.8%; Pred. No. 6.3e-218; Matches 563; Conservative 35; Mismatches 43; Indels
                                                                   6FAB16AF85107FE0 CRC64;
(GLCNAC. . .)
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R EMBL; AF038399; AAB9976.1; -
R EMBL; AF038399; AAB99976.1; -
R EMB; 1DF5; 26-JAN-00.
PDB; 1DF5; 26-JAN-00.
PDB; 1DF5; 26-JAN-00.
PDB; 1GC1; 19-ABG-90.
R PDB; 1GC1; 10-OCT-01.
PDB; 1GC1; 10-OCT-01.
R PDB; 1K31; 10-OCT-01.
R R InterPro; IFR000328; ENV GP41.
R InterPro; IFR000328; ENV GP41.
R Pfam; PF00516; GP120; 1.
R Pfam; PF00517; GP41; 1.
R AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Sign ADF.
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                                                                   Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.,
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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             MEDLINE=85111123; PubMed=2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R. Josephs S.F., Doran E.R., Ratlaki J.A., Whitehorn E.A., Laudenister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo lwong-Staal F.;
Complete nuclectide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1985).
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PDB; IDDH; 13-JAN-99.
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PDB; IQO3; 02-JAN-00.
PDB; ISZT; 24-DEC-97.
HIV; K02011; ENVSBHB.
GlycoSuiteDB; P04582; -
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Query Match 84.0%; Score 2918; DB 1; Best Local Similarity 82.2%; Pred. No. 1.4e-217; Matches 562; Conservative 35; Mismatches 43;
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF536757; AAN05642.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR0000738; EW, GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11676;
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     Conservative
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STRAIN=SHIVSF162P3.2;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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MEDLINE=2268496; PubMed=12743293;
MEDLINE=2268496; PubMed=12743293;
Robbins K. Lemeny P., Pybus O.G., Jaffe H.W., Youngpairoj Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of "U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of 'U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of 'U. Virol. 77:6359-6366(2003).

J. Virol. 77:6359-6366(2003).

EMBL: AX24722; AAP37150.1; -.

EBNP: BENCHORD FOOTER BS4 AA, 97048 MW; 36379231FF3AF12C CRC64;
                                                                                         LTPLCVTLHCTNLKNATNTKSSNWKEMDRGEIKNCSFKVGAG----
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Matches 584; Conservative
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NCBI_TaxID=11676;
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MEDLINE-22628496; PubMed=12743993;

MEDLINE-22628496; PubMed=12743993;

MEDLINE-22628496; PubMed=12743993;

MEDLINE-22628496; PubMed=12743993;

Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;

"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of Orig
Population History, and Characterization of Early Strains.";

J. Virol. 77:6559-666(2003)

EMBL; AX247221; AAP371499.1;
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86.1%; Pred. No. 3.3e-245;
iive 26; Mismatches 35; Indels 33;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Warches 584; Conservative
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STRAIN=81GA;
STRAIN=81GA;
ROBDINE=22628496; PubMed=12743293;
Robbins K.B., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
                               860;
                                                            41;
                               15; Length
                            cch 89.0%; Score 3092.5; DB 15; Lengt al Similarity 84.4%; Pred. No. 7.2e-245; 580; Conservative 29; Mismatches 37; Indels
 97762 MW; A7E185F2BD421590 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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            MRVKGIRKOYQHLWRGGTLLLCMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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MEDLINE=22658496; PubMed=12743293; Jaffe H.W., Youngpairoj A Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A Brown T.W., Salemi M., Vandamme A.M., Kalish M.L.;
"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of C Population History, and Characterization of Early Strains."; J. Virol. 77:6359-6366(2003).
EMBL; AY247218; AAP37146.1; -.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Envelope glycoprotein.
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                              STRAIN-81CA2;
MEDLINE-22624966; PubMed=12743293;
MEDLINE-22624966; PubMed=12743293;
MEDLINE-22624966; PubMed=12743293;
MEDDINS E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj
Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of
"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of
"U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of
"U.S. Human Transparence of Type 1 Type 2 
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                                                                                                                                                                                                                                                                                88.5%; Score 3074; DB 15;
84.9%; Pred. No. 2.3e-243;
live 32; Mismatches 31;
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01-JAN-1998 (TrEMBLrel. 05, L:
01-JUN-2003 (TrEMBLrel. 24, L:
Env polyprotein.
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580; Conservative
              FROM N.A
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                                                                                                                                                                                                                       Gaps
              Origin,
                                                                                                                                                                                                                       35;
                                                                                                                                                                      Query Match
88.6%; Score 3079.5; DB 15; Length 852;
Best Local Similarity 85.3%; Pred. No. 8.3e-244;
Matches 580; Conservative 27; Mismatches 38; Indels 35;
Population History, and Characterization of Barly Strains.", J. Virol. 77:6359-6366(2003).

EMBL: AV247220; AAP37148.1; -.
                                                                                                                              CRC64;
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676;
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                                                                                                                              852 AA; 96680 MW; F8D811028025D998
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01-OCT-2003 (TERMLrel.
Envelope glycoprotein.
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SEQUENCE 852 AA
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181 PIDNNSTRYRLISCNTSVITQACPKVTFEPIPIHYCAPAGFAILKCKDKKFDGKGFCTNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of HIVI-PAR, a macrophage-tropic strain: cell tropism, virus/cell entry and nucleotide sequence of the envelope glycoprotean."; appropriate of the envelope glycoprotean."; appropriate of the envelope glycoprotean."; appropriate of the sequence of the envelope glycoprotean."; appropriate of 1993). GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0019031; C:viral envelope; IEA. InterPro; IPR000328; Env GP41. InterPro; IPR000328; Env GP41. InterPro; IPR00077; GP120. Pfam; PF00516; GP120. Pfam; PF00516; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93189881; PubMed=8446773;
Schmidtmayerova H., Gayet O., Guettari N., Bolmont C., Hirsch I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%; Score 3040.5; DB 15; Length 846; ilarity 84.6%; Pred, No. 1.3e-240; Conservative 31; Mismatches 44; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Glycoprotein; Polyprotein; Transmembrane
846 AA; 96490 MW; 3D561D5735F90C84 CRC64;
                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676,
                                                                                                                                                                                                                                                                   846 AA
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570; Conserv
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                                                                                                                                                                                 "Construction and characterization of a stable full-length macrophage-
tropic HIV type I molecular clone that directs the production of high
titers of progeny virions.";
AIDS Res. Hum. Retroviruses 12:191-194(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 854 AA; 97291 MW; 06C45E69103C6C12 CRC64;
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                                                                                                                          MEDLINE=56432129; PubMed=8835195;
Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
Martin M.A., Peden K.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF004394; AAB64170.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005199; Fstructural molecule activity; IEA.
InterPro; IPR000777; GP120.
                   :iency virus 1.
viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 3049.5; DB 1984.9%; Pred. No. 2.4e-241; ive 20; Mismatches 44;
                 virus
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Best Local Similarity 84.9°
Matches 580; Conservative
                 Human immunodeficiency
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                               Viruses; Retroid
NCBI TaxID=11676;
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                                                                                                                                                                                                                                         1 MRVKGIRKNYQHLWRGGTLLLGMLMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                            Coat protein; Glycoprotein; Polyprotein; Transmembrane, NCE 847 AA; 96160 MW; 022D5F24E04FB29F CRC64;
                                                                                                                                                                       Length
                                                                                                                                                                                                        Indels
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR00777; GP120.
Pfam; PF00516; GP120; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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                                                                                                                                                                 87.4%; Score 3035; DB 15;
85.4%; Pred. No. 3.7e-240;
live 29; Mismatches 38;
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                                                                                                                                                                                   al Similarity 85.4
577; Conservative
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 KIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIV
                                                            GKAMYAPPIRGOIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVV
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"HIV-1 env sequence variation in brain tissue of patients with AIDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen I.S.;

Jobal infection of the central nervous system by AIDS viruses with distinct cellular tropisms.";
Science 236:819-822(1987).
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PIR; T09448; T09448; GO: Concept To membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.
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Last sequence update)
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MEDLINE=91043044; PubMed=2172833;
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MEDLINE=92092169; PubMed=1684385;
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MEDLINE=87206194; Pubmed=3646751;
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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DPEIVMHSFNCGGEFFYCNTTQLFNSTWNDTSTWNNTGNGTITLPCRIKQIVNMWQEVG 416
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SITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGG 336
                                                                                                                                                                                      DPBIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNT--NGTITLPCRIKQIINRWQEVG 394
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MEDLINE=98178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
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84.3%; Pred. No. 2.3e-239;
ive 34; Mismatches 34; Indels
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
SIL TaxID=11676;
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                                                                                               MEDILINE=95194694; PubMed=7888189; Gao F., Yue L., Craig S., Thornton C.L., Robertson D.L., McCutchan F.E., Bradac J.A., Sharp P.M., Hahn B.H.; Genetic variation of HIV type 1 in four World Health Organization-sponsored vaccine evaluation sites: generation of functional envelope (Glycoprotein 160) clones representative of sequence subtypes A, B, C, and E. WHO Network for HIV Isolation and Characterization."; AIDS Res. Hum. Retroviruses 10:1359-1368(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evaluation sites: genetic screening, sequence analysis, and preliminary biological characterization of selected viral strains. WHO Network for HIV Isolation and Characterization."; AIDS Res. Hum. Retroviruses 10:1327-1343(1994).
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"Molecular cloning and analysis of functional envelope genes from "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G.WHO and NIAID Networks for HIV Isolation and Characterization.";
J. Virol. 70:1651-1657(1996).
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Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000728; Env GP41.
Fam; PR000777; GP120.
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Pred. No. 9.5e-240;
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SEQUENCE FROM N.A.
STRAIN=014;
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                                                                                                                                                                                                                                                                                                                                                                       STRAIN=014;
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GO, GO:0005198; F:structural molecule activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR000128; Env GP41.
InterPro; IPR000177; GAP_dhdrogenase.
InterPro; IPR000177; GP120.
Pfam; PF00516; GP120; 1.
PROSITE; PS0071; GAPDH; 1.
PROSITE; PS0071; GAPDH; 1.
RAIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 852 AA; 96545 MW; 3C7780DB0611E617 CRC64;
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"Diversity of the human immunodeficiency virus type 1 envelope "Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in San Francisco Men's Health Study participants.";
AIDS Res. Hum. Retroviruses 14:329-337(1998).
EMBL, AF025750, AAC40588.1; -.
GO; GO:0016621; C:integral to membrane; IEA.
GO; GO:0019038; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p.
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STRAIN=SFWHS2.9;
MEDLINE=98178716; PubMed=9519894;
MCDLINE=PRE., Sanders-Buell E., Salminen M.O., Carr J.K.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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                                      Gaps
Query Match
87.0%; Score 3022.5; DB 15; Length 852;
Best Local Similarity 83.1%; Pred. No. 4e-239;
Matches 564; Conservative 37; Mismatches 45; Indels 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein; Glycoprotein; Polyprotein; Transmembrane (CE 853 AA; 96830 MW; EC8BA4418F8AEC47 CRC64;
                                                                                                                           MEDLINE=98178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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T "Diversity of the human immunodeficiency virus type 1 envelope
T glycoprotein in San Francisco Men's Health Study participants.";
AIDS Res. Hum. Retroviruses 14:329-337(1998).
R GD: GO:0016021; C:integral to membrane; IEA.
GO: GO:0019031; C:integral to membrane; IEA.
GO: GO:0019031; C:viral cappaid; IEA.
GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. ..; IR GO: GO:0006196; F:glyceraldehyde-3-phosphate dehydrogenase (p. ..; IR GO: GO:0006198; F:glyceraldehyde-3-phosphate dehydrogenase (p. ..; IR GO: GO:0006198; F:glyceraldehyde-3-phosphate dehydrogenase (p. ..; IR InterPro: IPR000173; GP41.
R InterPro: IPR000173; GP41.
R InterPro: IPR000177; GP120.
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SEQUENCE 851 AA; 96516 MW; 1CDAC83EE6464531 CRC64;
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McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                             Envelope glycoprotein.
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                                                                                                                                                                        LSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLIC
                                                                                                                                                                                                                                                          TTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELD
RWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELY
                        KYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=RL42;
MEDLINE=9915084; PubMed=9491920;
Graf M., Shao Y., Zhao Q., Seidl T., Kostler J., Wolf H., Wagner R.;
"Cloning and characterization of a virtually full-length HIV type 1
genome from a subtype B'-Thai strain representing the most prevalent
B-clade isolate in China.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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84.0%; Pred. No. 1.1e-238;
ive 28; Mismatches 46; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS, Coat protein, Glycoprotein, Polyprotein, Transmembrane.
SEQUENCE 845 AA, 95963 MW, 9AF138531C5D7D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H., Wagner
databases.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graf M., Shao Y., Seidl T., Koestler J., Wolf J
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ (
EMBL, U71182; AAC05236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS Res. Hum. Retroviruses 14:285-288(1998)
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Matches 568; Conservative
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01-AUG-1998 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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LTPLCVTLNCTNLKNATNTSST----MEGGEIKNCSFNITTSIKTKVKDYALFYKVDVVP 176
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AAP60063 AAP60349 AAP61514 AAW89325 ABU63322 AAB10053

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HTLV-III Lymphaden

HTLV-III Sequence HIV-1 env Human lym HIV-1 coa HIV-1 env HIV gp41 HIV-1 NL4

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No.
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Immunizing an animal and eliciting an immune response against heterologous HIV-1 in an animal, involves administering an immunogen comprising modified HIV-1 envelope protein, or DNA or virus encoding the The present invention relates to methods for immunising an animal, preferably human, against heterologous human immunodeficitency virus type 1 (HIV-1), and eliciting a heterologous immune response to HIV-1 in that animal. The method comprises administering an immunogen having at least Human immunodeficiency virus type 1; HIV-1; gp140 envelope protein; second hypervariable region; V2; SF162deltaV2; SF162DV2; AIDS; acquired immunodeficiency syndrome; anti-HIV; mutant; mutein; immunogen. N-terminal mutant of modified HIV-1 SF162DV2 gp140 envelope protein. Human immunodeficiency virus 1; strain SF162 (clade B) /note= "Encoded by CAGCTC" Shrivastava I; (AARO-) AARON DIAMOND AIDS RES CENT Location/Qualifiers Ā AAU75156 standard; protein; 619 Claim 5; Fig 17; 62pp; English. 27-JUN-2001; 2001WO-US020483. 27-JUN-2000; 2000US-0214608P. 26-JUN-2001; 2001US-00891609. Stamatatos L, Barnett S, (first entry) WPI; 2002-130836/17. N-PSDB; AAS15499. Misc-difference WO200200250-A2 08-MAY-2002 03-JAN-2002 Synthetic AAU75156; protein. RESULT 1 AAU75156 

HIV prote Human Imm Env prote HIV-1 SOS HIV-1 JR-

gp120 fro Ancestral

Amino aci

ENV prote HIV-1 (AT HIV-1 (AT AIDS asso AIDS asso Protein #

env gene ARV-2 (9B

Sequence

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one modified HIV-1 envelope protein with a deletion in the second hypervariable (V2) region or its fragment, or DNA or virus encoding the modified HIV-1 envelope protein. The invention discloses the polymucleotide and amino acid sequences for the full-length HIV-1 entent of SF162DV2) The immunogene protein, and, for an N-terminal mutant of SF162DV2. The immunogene of the invention are useful for immunialing an animal against heterologous HIV-1 strains by eliciting neutralising antibodies or protective antibodies in the animal. The method can be used to treat acquired immunodeficiency syndrome (AIDS). The present sequence represents the N-terminal mutant (deletion of amino acids 1-27) of modified HIV-1 SF162DV2 gp140 envelope protein
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100.0%; Pred. No. 8.8e-162;
iive 0; Mismatches 0;
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Modified full-length HIV-1 SF162DV2 gp140 envelope protein.

(first entry)

08-MAY-2002

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AAU75155;

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AAU75155 standard; protein; 646

RESULT 2 AAU75155

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The present invention relates to methods for immunising an animal, preferably human, against heterologous human immunodeficiency virus type 1 (HIV-1), and eliciting a heterologous immuno esponse to HIV-1 in that animal. The method comprises administering an immunogen having at least one modified HIV-1 envelope protein with a deletion in the second hyperoxariable (V2) region or its fragment, or DNA or virus encoding the modified HIV-1 envelope protein. The invention discloses the polymucleotide and amino acid sequences for the full-length HIV-1 expended and manion acid sequences for the full-length HIV-1 mutant of SPIG2DV2. The immunogens of the invention are useful for immunising an animal against heterologous HIV-1 strains by eliciting neutral ising antibodies or protective antibodies in the animal. The method can be used to treat acquired immunodeficiency syndrome (AIDS).
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Human immunodeficiency virus type 1; HIV-1; gp140 envelope protein; second hypervariable region; V2; SF162deltaV2; SF162DV2; AIDS; acquired immunodeficiency syndrome; anti-HIV; mutant; mutein; immunogen.
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Pred. No. 9.1e-162;
0; Mismatches 0;
                                                                       Human immunodeficiency virus 1, strain SF162
                                                                                                                                                             /note= "Encoded by CAGCTC'
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26-JUN-2001; 2001US-00891609.
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Gaps

28;

120 142 153 202 213 262 273 322 333 382 393 442 453 502 512 562 572 622

82 9

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expression cassette; HIV Gag; Env; Int; Nef; pl5RnaseH; Pol; Tat; Prot; Rev; HIV type C; gene therapy; vaccine; immunisation; HIV.
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                                                                                                                                                                                          SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPOEIVLEN
                                                                                                Length 842;
       on 23-OCT-2003 to standardise OS field)
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                                                                                                                                            Indels
                                                                                              Score 3275; DB 6;
Pred. No. 5e-159;
0; Mismatches 3;
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95.2%;
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                                                                                                                 Local Similarity .- nes 616; Conservative
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    isolates. (Updated
                                                  Sequence 842 AA;
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Matches 616
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                          327
                                                                        IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQII 360
                                                                                                                      387
                                                                                                                                                                                                             447
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IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNWTIGPNNTNGTITLPCRIKQII
                                                                                                                                                                                                                                                                                    448 YKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
                                                                                                                                                                                                                                                                                                                                                                                  LLSGIVQQQNNLLRAIBAQQHLLQLTVWGIKLQARVLAVERYLKDQQLLGIWGCSGKLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 TTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELD
                                                                                                                                                               NRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL
                                                                                                                                                                                                                                                         YKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
                                                                                                                                                                                             NRWQEVGKAMYAPPIRGQIRCSSNITGLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL
                                                                                                                                                                                                                                                                                                                                                     LLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKLQARVLAVERYLKDQQLLGIWGCSGKLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; gag; nef; prot; tat; rev; vif; vpr; vpu; env; anti-HIV; vaccine; immune response.
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16-JAN-2002; 2002US-0349728P
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18-AUG-2003
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Worst immunostice mount amino acid deleted or replaced in the region corresponding to residues 420-436 or 119-123 and 199-210 relative to isolate HXB-2 are disclosed. The modified Env polypeptide is based on HIV strain SP162, with numbering relative to isolate HXB-2. The Env polypeptides are modified so as to expose at least part of the CD4 polypeptides are modified HIV Env polypeptides, coding polymucleotides and constructs, further comprising an adjuvant, are used for inducing an immune response in an individual. The method involves administering a first composition comprising a polymucleotide encoding the Env polypeptide in a priming step and administering a second composition comprising a modified Env polypeptide as a booster in an amount conficient to induce an immune response in the individual. The first and/or second composition further comprises an adjuvant (claimed). The intracellularly produced Env polypeptides can be used for a number of diagnostic and therapeutic purposes to determine the presence of reactive antibodies/and or Env proteins in a biological sample to aid in the diagnosts of HIV infection or disease status or as measure of response to immunization. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel modified HIV Env polypeptides useful as immunizing agents and for preparing a vaccine to elicit an immune response against a broad range of HIV subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic modified human immunodeficiency virus (HIV) envelope
                         563 QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNWTWMEWEREID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1; vaccine; anti-HIV; immunogenic; modified; envelope; Env; CD4 binding region; V1/V2 loop; bridging sheet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.4%; Score 3275; DB 3; Length 847; Best Local Similarity 95.2%; Pred. No. 5e-159; Matches 616; Conservative 0; Mismatches 3; Indels 21
                                                                                                                   NYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1; isolate SF162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 115-117; 139pp; English.
                                                                                                                                                                                                                                                       AAY97073 standard; protein; 847 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin E;
                                                                                                                                                                                                                                                                                                                                                                                                                Variant HIV-1 SF162 Env gp160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200039303-A2
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31-OCT-2000
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    513
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                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel expression cassette comprising a polymucleotide sequence encoding a polypeptide including an HIV Gag, Enr. Nef, piSRnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscosally, intranasally, subcutaneously, intradermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is useful for immuniaation, generating packaging cell lines and producing HIV polypeptides. This sequence represents an HIV Type C related protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAVEKLWYTYYYGVPVWKEATTTLFCASDAKAYDTBVHNVWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                                                                                 encoding
                                                                                                                                                                                       Ξ;
                                                                                                                                                                                                                                                                     New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, plsRnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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                                                                                                                                                                                       Van Rensburg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3275; DB 7; Length 842;
Pred. No. 5e-159;
0; Mismatches 3; Indels 2:
                                                                                                                                                                                       Engelbrecht S,
                                                                                                                                                                                          Lian Y,
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 301pp; English.
                         05-JUL-2001; 2001US-0303192P.
31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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95.2%;
                                                                                                                                                                                          Zur Megede J, Barnett SW,
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                                                                                                                     (CHIR ) CHIRON CORP.
(UYST-) UNIV STELLENBOSCH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation;
                                           VIENFUMWEGNIMVEGWHEDIISLMDQSLKPCVKLTPLCTTHCTNLKGNATNTKSSNWKEM
                                                                                                                          VVIRSENFTDINAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH
-----KLINCNTSVITQACPKVS
                                                                                     WIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH
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                                                                                                               FEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEG
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31-AUG-2001; 2001US-031686PP.
16-JAN-2002; 2002US-0349732P.
16-JAN-2002; 2002US-0349871P.
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                                                                        DRGEI KNCSFKVGAG----
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                                                                                                     New synthetic polynucleotides encoding antigenic HIV type B and/or type C bylypettides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
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                                                                                                                                                                                                                         The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immunocenses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This is the amino acid sequence of a human immunodeficiency virus (HIV) envelope (env) protein
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                                                                                                                                                                                               Disclosure; Fig 2A-C; 262pp; English.
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(CHIR ) CHIRON CORP.
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This protein is the gpl20 (envelope glycoprotein) from the GNEB isolate of HIV-1 (human immunodeficiency virus type 1). There are neutralising epitopes in the V2 and C4 domains of gpl20, in addition to the neutralising epitopes in the V3 domain. Although the amino acid sequences
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263 VVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSTTIGPGRAFYATGDIIGDIRQAH
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                                                                                                    CNISGEKWANTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF
                                                                                                                     CNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPBIVMHSFNCGGEFFYCNSTQLF
                                                                                                                                                            334 NSTWINTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
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                                                                                                                                                                                                                                                                                                                                                                  563 QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREID
                                            VVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR67724 standard; protein; 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berman PW, Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-036112/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ76018
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25-MAR-2003
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                  203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL33942 to ABL40054 and ABB062015 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                        Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; immunostimulant; gene therapy.
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                  699
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 Van Rensburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3260; DB 5;
Pred. No. 2.9e-158;
0; Mismatches 6;
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                                                                                                                                                                              HIV Env isolate SF162 amino acid sequence.
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                                                                                                                                                                                                                                                                    Human immunodeficiency virus; type
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                                                                                         842
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Best Local Similarity 94.7%;
Matches 613; Conservative
                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2001; 2001WO-US021241
                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2000; 2000US-00610313
                                                                                         ABB06211 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SW,
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zur Megede J, Barnett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 842 AA;
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                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                      ABB06211;
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Human immunodeficiency virus 1.

WO200160838-A2

23-AUG-2001

16-FEB-2001; 2001WO-US005288 18-FEB-2000; 2000US-0183659P

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of the neutralising epitopes in the V2, V4 and C4 domains are variable, the amount of variation is highly constrained. This facilitates the design of HIV subunit vaccines that can induce antibodies that neutralise the most common HIV strains for a given geographic region. This invention provides a multivalent gpl20 subunit vaccine where the gpl20 present in the vaccine is from at least two HIV isolates which have different amino acid sequences for a neutralising epitope in these regions. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                    VIENFNIMMYNDOMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLKNATNTTSSSWGKM 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLTRDGGKEISNTTEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREK 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS-----TWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITG
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                                                                                                                                                                                         Length 850;
                                                                                                                                                                                                                        32; Indels
                                                                                                                                                                                         DB 2;
                                                                                                                                                                                        88.4%; Score 2942.5; DB 2
85.3%; Pred. No. 4.2e-142;
iive 27; Mismatches 32;
                                                                                                                                                                                                                        Matches 557; Conservative
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                                                                                                                                                              Sequence 850 AA;
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Preparing an ancestral viral amino acid sequence useful as a vaccine comprises determining a recent ancestor of a circulating virus by maximum

Claim 8; Page 54; 89pp; English

comprises determining a recentlikelihood phylogeny analysis.

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퓽 Learn

Rodrigo AG,

Mullins JI,

WPI; 2001-536565/59. N-PSDB; AAH26468.

UNIW ) UNIV WASHINGTON

The present sequence is that of an ancestral HIV-1 group M, subtype B and ancestral viral gene sequences and ancestral viral protein sequence for highly diverse viruses, such as HIV-1. The cuthods use samples of circulating viruses to determine an ancestral coviral sequence by maximum likelihood phylogeny analysis. In the present case, the ancestral HIV-1 subtype B env sequence (see AAH56468) was determined using 38 subtype B sequences (obtained from 9 different countries) and 3 subtype D (outgroup) sequences. The distances between this ancestral viral sequence and circulating strains used to determine to average 12.3% (range: 8.0-21.0%) while the available specimens were 17.3% different from each other (range: 13.3-23.2%). Thus, the consensus sequence was, on average, more closely related to any given circulating virus than to any other variant. The ancestral gpi60 sequence circulating virus than to any other variant. The ancestral gpi60 sequence consensus amino acids were represented. Thus, an immunogenic composition conto this subtype B ancestor protein will elicit broad neutralising antibody against HIV-1 isolates of the same subtype, and will also elicit consensus amino confines mediated by antigen sepecific T-cells. A claimed vaccine composition comprises a viral ancestor protein or its immunogenic fragment, especially one derived from the HIV-1 group M subtype B gp160 concentral protein. (Updated on 11-5EP-2003 to standardise OS field) 61 VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTN--LKNATNTKSSN-- 116 VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDDLRTNATNTTNSSAT 147 208 YRLINCNTSVITQACPKVSFEPIPIHYCTPAGFAILKCNDKKFNGTGPCTNVSTVQCTHG 267 148 TNTTSSGGGTMEGEKGEIKNCSFNVTTSIRDKMQKEYALFYKLDVVPIDNDNNNTNNNTS 1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN 28 SAAEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLEN -----WKEMDRGE1KNCSFKVGAG------ - KLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHG 88.0%; Score 2928; DB 4; Length 883; 83.3%; Pred. No. 2.4e-141; 569; Conservative 16; Mismatches Local Similarity Sequence 883 AA; 88 117 Query Match Matches g 셤 셤 ð ઠે ò ठे AAB82761 standard; protein; 883 AA

10;

64;

Indels

9 87 207

194

254

268 IRPVVSTQLLLNGSLAEBEVVIRSENFTDNAKTIIVQLNESVEINCTRPNNNTRKSIPIG 327

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HIV-1; env gene; gp160 protein; ancestral gene; phylogeny; vaccine.

Ancestral HIV-1 group M, subtype B gp160 protein.

(first entry)

(revised)

11-SEP-2003 29-OCT-2001

AAB82761;

IRPVVSTQLLLNGSLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIG

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RESULT 11
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                           312
                                                              PGRALYATGKIIGDIRQAHCNLSRAKWNYTLKQIVTKLREQFGNNKTTIVFNQSSGGDPE 387
                                                                                                                                                      RWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGG--KEISNT-TEIFRPGGGDMRDNWRS 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the influence of variation in host genes on the selection of microorganisms with protein substitutions, comprises typing individuals of a cohort infected with a microorganism for an intrinsic polymorphic
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                                                                                                                                                                                                                                                                                                                                          ARQLISGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQEL
                                                                                                                                                                                                                                                                                                                                                                                                                ARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSG
                           PGRAFYATGD11GD1RQAHCN1SGEKWNNTLKQ1VTKLQAQFGNK--T1VFKQSSGGDPE
                                                                                                                                                                                                                                                  MWQEVGKAMYAPPISGQIRCSSNITGLLTRDGGNNENTNNTDTEIFRPGGGDMRDNWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic marker; host response; HIV; AIDS related virus; vaccine; hepatitis related virus; HCV; HBV; drug resistance; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a HIV envelope protein.
                                                                                                                        IVMHSFNCGGEFFYCNSTQLFNSTW--NNTIGPNNT
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ABR55495
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pathogenic traits in a host, such as bacteria, fungi, mycobacterium, viruses and virus-like particles; for examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the hepatitis related viruses such as HCV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism where the drug affects the replication of the microorganism at the nucleotide or amino acid level. The present sequence represents a HIV envelope protein, which is expected to provide optimal cytotoxic T lymphocyte (CTL) induced therapeutic protection to the cohort examined in
                                                                                                                                                                                                                                                                                                                                                                        o,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 QAHCNISRAEMNYILKQIVKKIREQFGKNKTIVPNQSSGGDPEIVMHSFNCGGEFFYCNT 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 SFEPIPIHYCAPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 TQLFNSTWNNSTWNTEESNNTEGNETITLPCRIKQIINWWQEVGKAMYAPPIRGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VTENFNAMKNNNVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNT-KSSNWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 VTENFNWWYNNWVEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDLANDTNTNNTSGSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GVVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSIT--IGPGRAFYATGDIIGDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAHCNISGEKWNNTLKQIVTKLQAQFG-NKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQLFNSTWN----NTIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIBPLGVAPTKAKRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                           Length 856;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                      ch 87.7%; Score 2919; DB 6; al Similarity 85.1%; Pred. No. 6.7e-141; 559; Congervative 25; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ż
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                  Sequence 856 AA;
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25-MAR-2003
15-NOV-1990
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Best Local S:
Matches 559
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ID AAP8
XX AAC AAP8
AC AAP8
DT 24-C
DT 25-M
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451 TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 9; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 90US-00599491
93US-00022835
                                                                                                                                                                                                                                                                                                                                                             95US-00388809
                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 855 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT58551
                                                                                                                                                                                                                                                                                                                                                              15-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1990;
                                                                                                                                                                                                  17-OCT-2003
                                                                                                                                                                                                            25-MAR-2003
25-MAR-1997
                                                                                                                                                                                                                                                                                                                    US5576000-A
                                                                                                                                                                                                                                                                                                                                          19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                               Markham PD;
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                                                                                                                                                                               AAW11581;
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                                                                                                                                                                                                                                                                              vaccine.
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                                                                                                                                      RESULT 12
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                                                                                                                                                           The sequence is the result of cloning a hybrid envelope gene from HIV variants BH10 and RF. A central portion of the RF gene was used, the rest being from te distantly related variant BH10. The resulting clone, pAcHT6 produces a hybrid gp 160 envelope protein with novel immunological and antigenic characteristics. It may be used to as a vaccine and for diagnosis and therapy of AIDS. See also AAR80366. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIENPNAMKNDWVEQMHEDIISLWDQSLKPCVKLTPLCVSLKCTDLKNDTNTNSSSGRMI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNSTWNNTIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRDGGEDTTNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQL 332
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                                                                                                                                                                                                                                  - useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLLNGSLAEE
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                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 851;
                                                                                                                                                                                                                                Prodn. of recombinant HIV envelope proteins in insect cells vaccine against AIDS and for diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
                                                                                                                                                                             Jellis CL;
                                                                                                                                                                                                                                                                                                                                                                                           87.4%; Score 2908.5; DB 1, 83.8%; Pred. No. 2.3e-140; iive 38; Mismatches 36;
                   HIV; HT6; gp160; envelope protein; RF; AIDS.
                                        Human immunodeficiency virus; variant RF.
                                                                                                                                                                             Putney S,
                                                                                                                                                                                                                                                                Disclosure; Page ?; 4pp; English.
                                                                                                                                                                             Lynn D, Carson H,
                                                                                                     87EP-00310967
                                                                                                                          86US-00941111
                                                                                                                                     87US-00091481
                                                                                                                                                                                                                                                                                                                                                                                                                545; Conservative
                                                                                                                                                       (REPK ) REPLIGEN CORP.
                                                                                                                                                                                                 WPI; 1988-176944/26.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                            N-PSDB; AAN80948
                                                                                                                                                                                                                                                                                                                                                                         Sequence 851 AA;
HIV protein HT6
                                                                                                     14-DEC-1987;
                                                                                                                         15-DEC-1986;
                                                                                                                                     31-AUG-1987;
                                                                                 29-JUN-1988
                                                             EP272858-A.
                                                                                                                                                                             Rusche J,
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                                                                                                    569
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                                                                                                                                         569 KQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNMTWMEWDR
511 K-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acquired immune deficiency syndrome; AIDS; envelope protein; env
                                                                                                                                                                                                                                      Match 86.5%; Score 2876.5; DB 2; Length 855; Local Similarity 82.7%; Pred. No. 9.7e-139; es 542; Conservative 33; Mismatches 43; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Immunodeficiency Virus-1 strain BA-L envelope protein.
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                                                                                                                                NSTQLFNSTWNNTIGPNNT--NGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNI 385
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                                                                             ACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNG
                                                                                               SLAEEGVVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIG
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                                                                                                                                                                                                                                                      MEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                                                                                                                                                                            Env protein of the BA-L strain of Human immunodeficiency virus

    HIV-1 strain BA-L; env protein; vaccine; immunotherapy;
infection; immunogen; HIV-1 diagnosis.

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93US-00022835.
95US-00388809.
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25-FEB-1993;
15-FEB-1995;
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09-APR-1999
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                                                                                                                                                                                                                                                                       The present sequence represents the envelope protein of the BA-L (ATCC 40890) strain of Human immunodeficiency virus type 1 (HIV-1) strain MN-STI. BA-L is more typical of United States isolates of HIV-1 than previously known strains. Recombinant, complete env protein of the BA-L strain is used as a vaccine component and for immunotherapy of existing HIV infections, to detect HIV-specific antibodies, e.g. in donated blood, and as an immunogen to raise specific antibodies, for HIV-1 diagnosis. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                   DNA encoding env protein of the human immune deficiency virus isolate I
L - useful for producing protein for use in vaccines, as assay reagent
and to generate antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 NAEBKLMVIVYYGVPVWKEATITLFCASDRKAYDTEVHNVMATHACVPTDPNPQEVBLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIG
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                                   Popovic
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7
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DEPT HEALTH & HUMAN SERVICES
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                                     MS,
                                     Reitz
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Best Local Similarity 82.77
Matches 542; Conservative
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                                     Franchini
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N-PSDB; AAX04767.
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512

359 393

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Novel stable HIV-1 pre-fusion envelope glycoprotein trimeric complex in which each monomeric unit of the complex comprises HIV-1 gp120 and HIV-1 gp41, useful for eliciting immune response in subject against HIV-1.
                                                                               360 TWNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
                                                                                                                                                                                                                                                                            479 AVFLGFLGAAGSTWGAASMTLTVQARLLLSGIVQQQNNLLRAIEAQQRWLQLTVWGIKQL
216 IRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCN
                  240 IRSDNFTNNAKTIIVOLKESVEINCTRPNNNTRKSIHIGPGRAFYTGEIIGDIRQAHCN
                                                              276 ISGEKWINTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNS
                                                                                                                             TW-NNTIGPNNTNG-TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
                                                                                                                                                                                           394 GGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLG
                                                                                                                                                                                                                                                          454 AMFLGFLGAAGSTWGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-L
                                                                                                                                                                                                                                                                                                                          513 QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus; envelope glycoprotein trimeric complex;
HIV; anti-HIV; vaccine; immune response; HIV infection; gp120; gp41;
gp140; furin-recognition sequence.
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2001US-0317909P.
2001US-0317910P.
2002US-0370264P.
2002US-0370410P.
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06-SEP-2001;
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05-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a viral envelope protein. The viral envelope protein comprises a viral surface protein (e.g. glycoprotein gpl20) and a corresponding viral transmembrane protein (e.g. gpl1), in which the viral envelope protein contains one or more amino acid sequence mutations that enhance the stability of the complex formed between the viral surface and transmembrane proteins. The viral envelope protein enbe used in the treatment of viral infection e.g. HIV-1 infection. The present sequence is HIV-1 SOS gpl40, which was used in the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New viral envelope proteins, useful for producing vaccines to treat human immunodeficiency virus-1 infections, comprises amino acid sequence mutations such that viral transmembrane-surface protein complex is more stable.
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                                                                                                                                                                                                       gp120; anti-HIV; gene therapy; vaccine; viral envelope protein; gp41;
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84.5%; Pred. No. 4.2e-138;
iive 25; Mismatches 43;
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                                                            standard; protein; 643
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(first entry)
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Best Local Similarity 84.59
Matches 545; Conservative
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05-APR-2001
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The present invention describes a stable in pre-lation envisible of a propriet of the present invention describes a stable in pre-lation in the proposed of th present invention describes a stable HIV-1 pre-fusion envelope X2222222222222222222222X8

Sequence 643 AA;

Gaps 32; Length 643; Indels 86.0%; Score 2862; DB 6; 84.5%; Pred. No. 4.2e-138; iive 25; Mismatches 43; Best Local Similarity 84.5 Matches 545; Conservative Query Match

9 VEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVT VEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLENVT

GEIKNCSFNITTSIRDEVQKEYALFYKLDVVPIDNNNTSYRLISCDTSVITQACPKISFE 179 GEIKNCSFKVGAG---------KLINCNTSVITQACPKVSFE 155

215 PIPIHÝCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVV 239 PIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEBGVV

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Search completed: February 25, 2004, 14:16:31 Job time : 54.8474 secs

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1 SAVEKLWTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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Sequence 23,
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Sequence 14,
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(c) 1993 - 2004 Compugen Ltd.
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S-08-487-14
S-07-95-110
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US-08-463-210-11
US-08-463-210-11
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US-08-482-847-14
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Patent No. 5864027
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION:
INVERTOR: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: MCOULChen, Doyle, Brown & Energen, LLP
STREET: 3 Embarcadero Center
CITY: San Francisco
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Best Local Similarity 85.3%; Pred. No. 8.1e-234;
Matches 557; Conservative 27; Mismatches 32;
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MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,603A
FLING DATE: 07-JUN-1994
FLING DATE: 07-JUN-1994
FLING DATE: 07-JUN-93
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REGISTRATION NUMBER: 38903
REGISTRATION NUMBER: 38903
TELEROMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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S-09-718-096-23
S-07-916-098A-2
S-08-472-240A-5
S-08-472-240A-10
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US-09-536-977-72
US-09-337-387-3
US-08-022-835-2
US-08-388-809-2
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US-07-956-483-11
US-08-472-240A-6
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US-08-388-809-4
US-08-647-714-4
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LENGTH: 850 amino acids
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STRANDEDNESS: si
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US-08-448-603A-28
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328 CNLSSTKWNNTLKQIVTKLREHF-NKTIVFNHSSGGDPEIVMHSFNCGGEFFYCNTTPLF 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 NS-----TWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 WEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
                                                                                                                                                                                                                                                  DB 3; Length 850;
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TITLE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     8.1e-234;
                                                                                                                                                                                                                                                88.4%; Score 2942.5; 85.3%; Pred. No. 8.1e-
                                                                                                                                                                                                                                                                                    27; Mismatches
              14918-704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berman, Phillip W.
           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2286
TELEFAX: 415-393-2286
38903
                                                                                                       28:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                     Best Local Similarity con-
Matches 557; Conservative
                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            STRANDEDNESS: single
REGISTRATION NUMBER:
                                                                                                                                                                                              linear
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US-09-492-739-28
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                                                   208 FEPIPIHYCAPAGFAILKCRDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEE 267
                                                                                                                                                                                                                                                  VVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH 273
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                                                                                                         DRGEIKNCSPKVGAG-------KLINCNTSVITQACPKVS 153
                                                                                                                                                                              FEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEG 213
28 SAAEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIGLEN 87
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                                   VTENFNAWKONNWVEQWHEDIISLWDQSLKPCVKLTPLCVTLTHCTNLKNATNTKSSNWKEM
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3 Embarcadero Center
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APPLICANT: Nakamura, Gerald R.
ITILE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enerse
STREET: 3 Embarcadero Center
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SOFTWARE: FRANCESEQ FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,075
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,603
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
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MEDIUM TYPE: Diskette
COMPUTER: IBM Competible
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US-09-134-075-28
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505 RAVGIGAVFLGFLGAAGSTMGAASVTLTVQARLLLSGIVQQQNNLLRAIEAEQHLLQLTV 564
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                                                                  28 SAAEQLWVIVYYGVPVWKEAITILFCASDAKAYDTEVHNIWATHACVPIDPNPQEVVLGN
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                                              508 WGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWME
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                                                                                                                               567 WEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                                                                        625 WEREIDNYTSLIYSLIEESQNQQEKNEQELLELDKWASLWNWFDITKWLWYIK 677
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                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: 97160 VARIANT
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CURRENT APPLICATION DATA:
PALLCATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.6%; Score 2880.5; DB 3; 83.3%; Pred. No. 1e-228; iive 31; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burne, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 NWKEMDRGEIKNCSFKVGAG-----
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Sequence 14, Application US/07956483
Patent No. 6261799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFRENCE/DOCKET NUMBER: 01775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
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Matches 547; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
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US-07-956-483-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 VVIRSANFSDNAKTIIVQLNESVEINCTRPNNNTRRSIHIGPGRAFYATGEIIGDIRQAH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIBAQQHLLQLTV 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIENFNAMAKNINVVEQMHEDIISLADQSLKPCVKLTPLCVTLNCTDLKNATNTTSSSWGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 SAAEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQBIGLEN
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      Doyle, Brown & Enersen, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.4%; Score 2942.5; DB 4
85.3%; Pred. No. 8.1e-234;
iive 27; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 14918-704
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,739
FILING DATE: 27-Jan-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/134,075
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
ADDRESSEE: McCutchen, Doyle,
STREET: 3 Embarcadero Center
                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 850 amino acids
                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                         CITY: San Francisco
STATE: CA
                                                                                                     ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.3
Matches 557; Conservative
                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-492-739-28
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TELEPHONE:
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US-08-388-809-6
                                                                                                                                                           Query Match
Best Local S:
Matches 542
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                               KVSFBPIPIHYCA-RWFAILNCNNKKFNGTGPCTNVSTVQCTHGIRPVVSTHLLLNGSLA 266
                                                                       270
                                                                                     QAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNST 330
                                                                                                                                               QLFNSTWNNTIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGL 388
                                                                                                                                                                                                        LLTRDGGKEISNT----TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRKVVQ 444
                                                                                                                                                                                                                                                                   REKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLL 503
                                                                                                                                                                                                                                                                                                                         QLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM 562
                                                                                                                                                                                                                                                                                                                                                                               567 QLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICTTTVPWNTSWSNKSLDKIWGNM 626
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                                                                       EEGVVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIR
                KVSFEPI PIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLA
                                                                                                                                                                                                                                                                                                                                                                                                                          TWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
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APPLICANT: Gallo, Robert C.
APPLICANT: Lori, Franco C.
APPLICANT: Popovic, Mikulas
APPLICANT: Garnter, Suzanne
TITLE OF INVENTION: MOLECULAR CLONES OF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDMER:
TLING DATE: 17-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/71
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/08022835; Patent No. 5420030; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reitz Jr., Marvin S.
Franchini, Genoveffa
Markham, Phillip D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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US-08-022-835-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 ACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGKGPCTNVSTVQCTHGIRPVVSTQLLLNG
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                                                                                                                                                                                                                                                                                                                                                             28 NAEEKLWYTVYYGVPVWKEATTTLFCASDRKAYDTEVHNVWATHACVPTDPNPQEVELKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 SLAEEGVVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 DIROAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 NSTQLFNSTWNNTIGPNNT--NGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 NSTQLFNSTWNVTEESNNTVENNTITLFCRIKQIINMWQEVGRAMYAPPIRGQIRCSSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 TGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 EKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 EKRAVGIGAVFLGFLGAAGSTMGAAAMTLTVQARLLLSGIVQQQNNLLRAIEAQQHLLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 TVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTW
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681
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                                                                                                                                                                                                                                             Length 855;
                                                                                                                                                                                                                                                                                         Indels
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Patent No. 557600
GENERAL INFORMATION:
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
APPLICANT: GARTHER, SUZANNE
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                           86.5%; Score 2876.5; DB 1
82.7%; Pred. No. 2.2e-228;
                                                                                                                                                                                                                                                                                         33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DR----GEIKNCSFKVGAG------
             TELERAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 855 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-022-835-6
(202) 861-3000
                                                                                                                                                                                                                                                                    al Similarity 82.79
542; Conservative
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507 EKRAVGIGAVFLGFLGAAGSTMGAAAMTLTVQARLLLSGIVQQQNNLLRAIEAQQHLLQL 566
                                                                 567 TVWGIKQLQARVLAVERYLEDQQLLGIWGCSGKLICTTAVPWNASWSNKSLNKIWDNMTW
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                                          506 TVWGIK-LOARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTW
                                                                                                                                                Indels 37; Gaps
                                                                                                                         565 MEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 855;
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,

APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT

APPLICANT: GENTY FRANCO C.; POPOVIC, MIKULAS; AND

APPLICANT: GARTNER, SUZANNE

TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.5%; Score 2876.5; DB 2; Best Local Similarity 82.7%; Pred. No. 2.2e-228; Matches 542; Conservative 33; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRILING DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4092US2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK, 3.5"
                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/08647714 ; Patent No. 5869313
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CITY: NEW YORK
STATE: NEW YORK
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acid
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US-08-647-714-6
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,809

FILING DATE: 15-FEB-1995

PRIOR APPLICATION NUMBER: US 08/022,835

FILING DATE: 25-FEB-1993

APPLICATION NUMBER: US 07/599,491

FILING DATE: 17-0CT-1990

ATOMNEY AGENT INFORMATION:

NAME: LESLIE A. SERUNIAN

REGISTRATION NUMBER: 30.36-4092US2

TELEPHONE: (212) 756-4800

TELEPHONE: (212) 756-4800

TELEPHONE: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEC ID NO: 6:
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82.7%; Pred. No. 2.2e
tive 33; Mismatches
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              T: 345 PARK AVENUE
NEW YORK
:: NEW YORK
RY: USA
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amino acid
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                                                                                           ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
ADDRESSEE: MORGAN
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Best Local S:
Matches 542
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APPLICANT: BALLAUN, Claudia
APPLICANT: TRKOLA, Alexandra
APPLICANT: TRKOLA, Alexandra
APPLICANT: REME, Renate
APPLICANT: SCHWAT2, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: STEINOL, Franz
APPLICANT: STEINOL, Franz
APPLICANT: MUSTER, Thomas
ITILE OF INVENTION: HIV-Vaccines
TITLE OF INVENTION: HIV-Vaccines
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human imunodeficiency virus type
----GEIKNCSFKVGAG----
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SOFTWARE: PatentIn version 3.0
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BUCHACHER, Andrea
ERNST, Wolfgang
BALLAUN, Claudia
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NAME/KEY: PEPTIDE
LOCATION: (326)..(400)
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                                                                                     29 SATEKLMVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNWATHACVPTDFNPQEVVLVN
                                                                                                                                                61 VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKE-
                                                                                                                                                                      89 VIENFNAWKNDWVEQWHEDIISLWDQSLKPCVKLTPLCVSLKCTDLKNDTNTNSSSGRMI
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APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WANGE TO FLOSSIE
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
                        Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE PATENTIN DATA:
APPLICATION NDMER: US/08/463,210
FILING DATE: 05-JUN-1995
                        37;
83.4%; Pred. No. 2.8e-226; ive 32; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08463210 Patent No. 6001977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
  Best Local Similarity 83.4%
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan &
STREET: 345 Park Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-463-210-11
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1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 863;
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..863
OTHER INFORMATION: /note= "env protein of HTLV-III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 85.7%; Score 2851; DB 4;
Best Local Similarity 83.4%; Pred. No. 2.8e-226;
Matches 548; Conservative 32; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION 1935
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-0CT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leelie A.
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 3226-4193US3
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                               ; Sequence 11, Application US/08463028
; Patent No. 6610476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 863 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: HTLV-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                          US-08-463-028-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 SFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLABE 275
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Best Local Similarity 83.4%; Pred. No. 2.8e-226;
Matches 548; Conservative 32; Mismatches 37; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
LOCATION: 1..863
CTHER INFORMATION: /note= "env protein of HTLV-III"
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION WIMER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REFERENCE/DOCKET NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193USZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 863 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HTLV-III
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ORIGINAL SOURCE:
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       STRANDEDNESS:
TOPOLOGY: ur
US-08-127-499A-14
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US-08-482-847-14
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                                                                Query Match
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                                                                                                                                                                           TOLFNSTWNN----TIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS 383
                                                                                                                                                                                                                                  395 TQLFNSTWFNSTWSTKGSNNTEGSDTITLPCRIKQIINMWQEVGKAMYAPPISGQIRCSS 454
                                                                                                                                                                                                                                                                       NITGLLLIRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV 443
                                                                                                                                                                                                                                                                                                    513
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                                                                                                                                                                                                                                                                                                                                               QLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM 562
                                                                                                                                                                                                                                                                                                                                                                                                           574 QLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQIWNNM 633
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                                                                                                                                                                                                                                                                                          SFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08127499A

Patent No. 5510264

GENERAL INFORMATION:
APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardher
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BEACHILI Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/127,499A

FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REFRENCE/COMMUTATION INFORMATION:

TELECOMMULCATION INFORMATION:

TELECOMMULCATION INFORMATION:

TELECOMMULCATION INFORMATION:
MDRGEIKNCSFKVGA---GK------
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-127-499A-14
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Sequence 14, Application US/08482847

Patent No. 5556757

GENERAL INFORMATION:

APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF NUMBER OF SEQUENCES: 40

CORRESPONDENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
                                                                                                                                                                                                                                                                                                                     209 ACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 IRCSSNITGLLLTRDGGNN-NNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 KRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VIENFNAMFKNDMVEQMHEDIISLMDQSLKPCVKLTPLCVSLKCTDLGNATNTNSSNTNSS
                                                                                                                                                                                                                                                                                                                                                                           ACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITI--GPGRAFYATGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 SLAEEEVVIRSANFTDNAKTIIVQLNQSVEINCTRPNNNTRKSIRIQRGFGRAFVTIGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGDIRQAHCNISGEKWNNTLKQIVTKLQAQFG-NKTIVFKQSSGGDPEIVMHSFNCGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYCNSTQLFNSTWNN----TIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 IRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 IWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWY
                                                                                                                                  SAVEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                                                                                                                        SATEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVN
                                                                                                                                                                                                                   VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKE-
                                                                                             Gaps
                                                                                             45;
                                                     Length 861;
                                                                                           Indels
                                                                                           39;
                                                   85.6%; Score 2848.5; DB 1
82.8%; Pred. No. 4.5e-226;
ive 30; Mismatches 39;
                                                                                                                                                                                                                                                                                                  120 -----MDRGEIKNCSFKVGA---GK-
                                                                          Local Similarity 82.8
nes 548; Conservative
unknown
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686
                        567 QQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLEQ 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----MDRGEIKNCSFKVGA---GK-------LINCNTSVITQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 SGEMMAEKGEIKNCSFNISTSIRGKVQKEYAFFYKLDIIPIDNDTTSYTLTSCNTSVITQ 208
                                                                                                              558 IWNNMTWMEWEREIDNYTNLIYTLIEESQNQOEKNEQELELDKWASLWNWFDISKWLWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SAVEKLWYTYYYGVPVWKEATTTLFCASDAKAYDTEVHNWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOLUBLE AND UNCLEAVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.6%; Score 2848.5; DB 3
82.8%; Pred. No. 4.5e-226;
iive 30; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burne, Done, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STREET: Virginia COUNTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID,
TITLE OF INVENTION: GP160 VARIANT
                                                                                                                                                                                                                                                                                                                                                                          US-07-956-483-10
; Sequence 10, Application US/07956483
; Patent No. 6261799
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TELEPHONE: (703) 836-6620
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INFORMATION FOR SEQ ID NO:
SEQUENCY CHARACTERISTICS:
LENGTH: 861 amino acids
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548; Conservative
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CORRESPONDENCE ADDRESS:
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Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYCNSTQLFNSTWNN----TIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYCNSTÓLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQEVGKAMYAPPISGQ 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQ 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: O'-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 38-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 -----MDRGEIKNCSFKVGA---GK-
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.6
Best Local Similarity 82.8
Matches 548; Conservative
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                                                                      20007-5109
D.C.
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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INFORMATION FOR SEQ ID NO:
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                                                            SLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITI--GPGRAFYATGDI
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Patent No. 6284248
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: MOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: 9p160 VARIANT
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/472,240A FILING DATE: 0.7UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/956,483 FILING DATE: 31-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-055
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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(703) 836-2021
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                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                            85.6%; Score 2848.5; DB 3; 82.8%; Pred. No. 4.5e-226; iive 30; Mismatches 39;
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Patent No. 6284248
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID,
TITLE OF INVENTION: gp160 VARIANT
SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                               Best Local Similarity 82.8
Matches 548; Conservative
                                                                                                                                   NAME/KEY: Protein
; LOCATION: 1..854
US-08-472-240A-1
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                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A
FILING DATE: 07-JUN-1995
PLIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 07/956,483
FILING DATE: 31-DEC-1992
ATTORNEY/AGERT INFORMATION:
ANALY AGENT INFORMATION:
ANALY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----MDRGEIKNCSFKVGA---GK-----
                                     SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 861 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
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IOCATION:
US-08-472-240A-7
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Db 448 IRCSSNITGLLTRDGGNN-NNGSEIFREGGEDMRDNWRSELYKYKVVKIEFLGVAPTKA 506

Qy 439 KRRVVQREKRAVTLGAMFLGFLGAAGSTWGARSLTLTVQARQLLSGIVQQQNNLLRAIEA 498

Db 507 KRRVVQREKRAVGIGALPLGFLGAAGSTWGARSMTLTVQARQLLSGIVQQQNNLLRAIEA 566

Qy 499 QQLLQLTVWGIK-LQARVLAVBRYKLDQQLLGIWGCSGLICTTAVPWNASWSKSLDQ 557

Db 567 QHLLQLTVWGIKQLQARILAVBRYLKDQQLLGIWGCSGKLICTTAVPWNASWSKSLDQ 626

Qy 618 IW 619

Db 627 IWNNWTWMEWBREINNYTMLIYTLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWY 686

Qy 618 IK 619

Db 687 IK 688

Search completed: February 25, 2004, 14:20:12
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Sequence 103, Appl
Sequence 1, Appli
Sequence 15, Appli
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Sequence 2, Appli
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(without alignments)
4047.104 Million cell updates/sec
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                                                                                                                                                                                                                                                                          3327
1 SAVEKLWVTVYYGVPVWKEA.....DKWASLWNWFDISKWLWYIK 619
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-10-241-009-2

1 US-10-190-434B-2

1 US-10-190-305A-2

US-09-476-242-2

1 US-10-026-741-103

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US-09-476-242-1
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US-09-938-406-1
US-10-196-515-3
US-10-196-515-12
US-10-032-162-15
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US-09-891-609-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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; Pred. No. 2.8e-296;
0; Mismatches 0;
US-10-032-162-17
US-10-190-435-6
US-10-190-434B-6
US-10-190-434B-6
US-10-190-305A-6
US-10-286-332A-6
US-10-286-332A-3
US-10-286-332A-3
US-10-190-435-147
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US-10-190-435-138
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Best Local Similarity 100.0%;
Matches 619; Conservative 0
    \begin{array}{c} 8.67 \\ 8.67 \\ 9.69 \\ 9.69 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.67 \\ 9.
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                                                                                                                                                                 YKYKVVKI EPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQ
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                                                                   NRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSEL
                                                 IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNTIGPNNTNGTITLPCRIKQII
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| Sequence 2, Application US/2030143248A1
| Sequence 2, Application No. US20030143248A1
| GENERAL INFORMATION:
| APPLICANT: URR MEGEDE, Jan
| APPLICANT: ENGREBRECHT, Susan W.
| APPLICANT: ENGREBRECHT, Susan W.
| APPLICANT: ENGREBRECHT, Susan W.
| APPLICANT: USAN YING STREELING DOLYPETION: POLYPECTION: POLYPECTION: POLYPECTION: POLYPETION: STREEPING: PP18133.003 / 2302-18133
| CURRENT FILING DATE: 2002-12-30 | NUMBER OF SEQ ID NOS: 319 |
| SEQ ID NOS: 319 |
| SEQ ID NOS: 2002-12-30 |
| SEQ ID N
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US-10-190-435-2
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Pred. No. 2.6e-291;
0; Mismatches 3;
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Best Local Similarity 95.2%;
Matches 616; Conservative
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                                                                               241 TRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKT
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Patent No. US20020127238A1
GENERAL INFORMATION:
APPLICANT: Stamatatos, Leondias
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
FILE REFERENCE: 2570-1-002N
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
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TYPE: PRT
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US-09-891-609-2
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US-09-891-609-2
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     263 VVIRSENFIDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH 322
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                                                               323 CNISGEKWNNTLKQIVTKLQAQFGNKIIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF
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Sequence 2, Application US/10190434B
Publication No. US20030194800A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan
APPLICANT: LIAN, Ying
ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
ITILE REPERENCE: 2300-1621.20
CURRENT APPLICATION NUMBER: US/10/190,434B
CURRENT PLING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 842
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ORGANISM: Artificial Sequence
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Best Local Similarity 95.2<sup>3</sup>
Matches 616; Conservative
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Sequence 2, Application US/201010614A1
GENERAL INPORMATION:
APPLICANT: 2UR MEGEDE, Jan
APPLICANT: BARNETT, Susan
APPLICANT: BARNETT, Susan
TITLE OF INVENTION: POLYPERTIDES ENCODING ANTIGENIC HIV TYPE B
TITLE OF INVENTION: POLYPERTIDES, POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/241,009
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 842
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Best Local Similarity
Matches 616; Conserv
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268 VVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGFGRAFYATGDIIGDIRQAH 327
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CNISGEKWNNTLKQIVTKLQAQPGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF 333
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                                                                                              AMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIBAQQHLLQLTVWGIK-L
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                     CNISGEKWINTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVWHSFNCGGEFFYCNSTQLF
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APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION UNDHER: US/09/476,242
CURRENT APPLICATION UNDHER: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 250
LENGTH: 847
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Pred, No. 2.6e-291;
0; Mismatches 3;
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ORGANISM: Human immunodeficiency virus
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Sequence 2, Application US/09476242

; Petent No. US20020146683A1

; GENERAL INFORMATION:
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Best Local Similarity 95.2%;
Matches 616; Conservative
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                                                                                                                    383 NSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLITRD 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10190305A
Publication No. US20030196621A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: LIAM, Ying
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 2302-18702 / 18702.002
CURRENT PELLING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOOTWARE: PATCHIN USE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAVEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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                                           323 CNISGEKWNNILKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF
                                                                                                NSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
98.4%; Score 3275; DB 14; Length 842;
Best Local Similarity 95.2%; Pred. No. 2.6e-291;
Matches 616; Conservative 0; Mismatches 3; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                          623 NYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 669
                                                                                                                                                                                                                                                                                                                                                                                                      NYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
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US-10-190-305A-2
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ORGANISM: Artificial Sequence
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US-10-190-305A-2
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                                                                                                                                                                                          420 GGIN-ENGTEIFRPGGGDMRDNWRSEFYKYKVVKIEPLGVAPTKCKRRVVQREKRAVGIG
       336 TW-NNTIGPNNTNG-TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
                                               360 TWINNTEGSINTEGNITTLECRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLTRD
                                                                                                                                                  394 GGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLG
                                                                                                                                                                                                                                                                                      454 AMPLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-L
                                                                                                                                                                                                                                                                                                                           513 QARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWEREID
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WEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
COMPUTER
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ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 SUBTYPE) ANTIGENS
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REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUILLENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQELINE
COHEN, JAQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I Street, N.W. CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 103, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
GLAVEL, FRANCOISE
BORMAN, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunner, L.L.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J
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TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acid
TYPE: amino acid
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                                                                                                                                                                                          AMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-L 512
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| GEIKNCSFNITTSIRDEVQKEYALFYKLDVVPIDNNNTSYRLISCDTSVITQACPKISFE 179
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NSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD 393
                                                                                                                                                                                                                                                                                                                                                        AMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQL 567
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                                               GGKE1SNTTE1FRPGGGDMRDNWRSELYKYKVVK1EPLGVAPTKAKRRVVQREKRAVTLG
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APPLICANT: SCHUELKE, NORBERT
APPLICANT: OLSON, WILLIAM C
APPLICANT: OLSON, WILLIAM C
APPLICANT: JOHN, MODE P
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/032,162
CURRENT FILING DATE: 2002-10-24
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PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
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US-10-032-162-13
Sequence 13, Application US/10032162
Publication No. US20030052839A1
GENERAL INFORMATION
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| Sequence No. US20020146683A1
| GENERAL INFORMATION:
| APPLICANT: BARNETT, Susan
| APPLICANT: HARTOG, Karin
| TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
| FILE REFERENCE: 1605.002
| CURRENT FILING DATE: 1999-12-30
| CURRENT FILING DATE: 1999-12-30
| NUMBER OF SEQ ID NOS: 26
| SOFTWARE: Patentin Ver. 2.0
                                                                     Query Match
Best Local Similarity 82.8%; Pred. No. 3.8e-252;
Matches 548; Conservative 30; Mismatches 39;
                                   NO: 103
         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID US-10-026-741-103
 STRANDEDNESS: single
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Sequence 11, Application US/10196515; Publication No. US20030091594a1; Sequence 11, Application No. US20030091594a1; Publication No. US20030091594a1; GENERAL INFORMATION:

APPLICANT: HOOME, James A.; APPLICANT: DOMS, Robert W.; APPLICANT: HOFFMAN, Trevor L.; TITLE OF INVENTION: THENAPEUTICS; TITLE OF INVENTION: THENAPEUTICS; TITLE OF INVENTION: THENAPEUTICS; CURRENT APPLICATION NUMBER: US/10/196,515; CURRENT FILING DATE: 2002-07-16; PRIOR PEPLICATION NUMBER: US/09/337,387; PRIOR FILING DATE: 1999-06-22, PRIOR FILING DATE: 1999-06-24; PRIOR FILING DATE: 1999-06-24
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                                                                          tch 85.2%; Score 2834; DB 9; al Similarity 82.6%; Pred. No. 8e-251; 543; Conservative 33; Mismatches 41;
TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                              Query Match
Best Local Similarity
Matches 543; Conserv
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FREENT NO. US20020155120A1
GENERAL INFORMATION:
APPLICANT: Lowell, George
APPLICANT: Vancott, Thomas
APPLICANT: Birx, Deborath AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: INDUCING MUCOSAL IMMUNITY
FILE REFERENCE: 40646-20002.10
CURRENT APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 2001-08-21
FRIOR APPLICATION NUMBER: US/09/14,701
FRIOR RILING DATE: 1999-09-30
FRIOR APPLICATION NUMBER: CURRENT FILING DATE: 1999-09-30
                                                                                                     ; Score 2819; DB 14;
; Pred. No. 1.9e-249;
35; Mismatches 40;
                                                 TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                              120 MDRGEIKNCSFKVGA---GK-----
                                                                                                   Query Match
Best Local Similarity 82.5%;
Matches 542; Conservative 3:
          SOFTWARE: Patentin Ver. SEQ ID NO 11
NUMBER OF SEQ ID NOS:
                                                                           US-10-196-515-11
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                                                                                                                                                                                                                       DB 9; Length
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                 Query Match
84.6%; Score 2813.5; DB 9
Best Local Similarity 79.3%; Pred. No. 6.2e-249;
Matches 533; Conservative 36; Mismatches 44;
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: US 60/021,687
PRIOR FILING DATE: 1996-07-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 --WKEMDRGEIKNCSFKVGAG-----
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Publication No. US20030091594A1
GENERAL INFORMATION:
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APPLICANT: LABRANNER, Celia C.
APPLICANT: DOMS, Robert W.
APPLICANT: HOFFMAN, Trevor L.
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684 WSDITKWLWYIK 695
                                                                                                                                      ; TYPE: PRT
; ORGANISM: Virus HIV-1
US-09-938-406-1
                                                                                                                  LENGTH: 868
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DOMS, Robert W.
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                                                                                                                                                                                                                                                                                    29 NATEKLWYTVYYGVPVWKEATTTLFCASDAKAYETEVHNVWATHACVPTDPNPQEVVLVN 88
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   CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND THERAPEUTICS
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                                                                                                                                                                                                                    84.1%; Score 2797.5; DB 14; Length 726; 81.8%; Pred. No. 1.4e-247; ive 37; Mismatches 45; Indels 37;
                                                                                                                                                                      TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVEIT TITLE OF INVENTION: THERAPEUTICS
FILE REFERENCE: HOASE 9596-104U1 (0282)
CURRENT APPLICATION NUMBER: US/10/196,515
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: US/09/337,387
PRIOR FILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-24
NUMBER: OF SEQ ID NOS: 12
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 726
                                                                                                                                                                                                                                   Best_Local Similarity 81.8%
Matches 534; Conservative
                                                                                                                                                                                              US-10-196-515-3
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Sequence 12, Application US/10196515 Publication No. US20030091594A1 GENERAL INFORMATION:

US-10-196-515-12

APPLICANT: HOXIE, James A. APPLICANT: LABRANCHE, Celia C.

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APPLICANT: HOFFMAN, Trevor L.

TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND TITLE OF INVENTION: THERAPEUTICS
FILE REPERENCE: Hoxie 9596-10410 (0282)
CURRENT APPLICATION NUMBER: US/10/196,515
PRIOR PILING DATE: 1009-06-22
PRIOR PILING DATE: 1099-06-22
PRIOR FILING DATE: 1099-06-22
NUMBER OF SEQ ID NOS: 12
SCOTTWARE: PatentIn Ver: 2.1
SEQ ID NO 12
LENGTH: 759
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.0%; Score 2793.5; DB 14; Length 759; Best Local Similarity 81.9%; Pred. No. 3.5e-247; Matches 535; Conservative 36; Mismatches 45; Indels 37;
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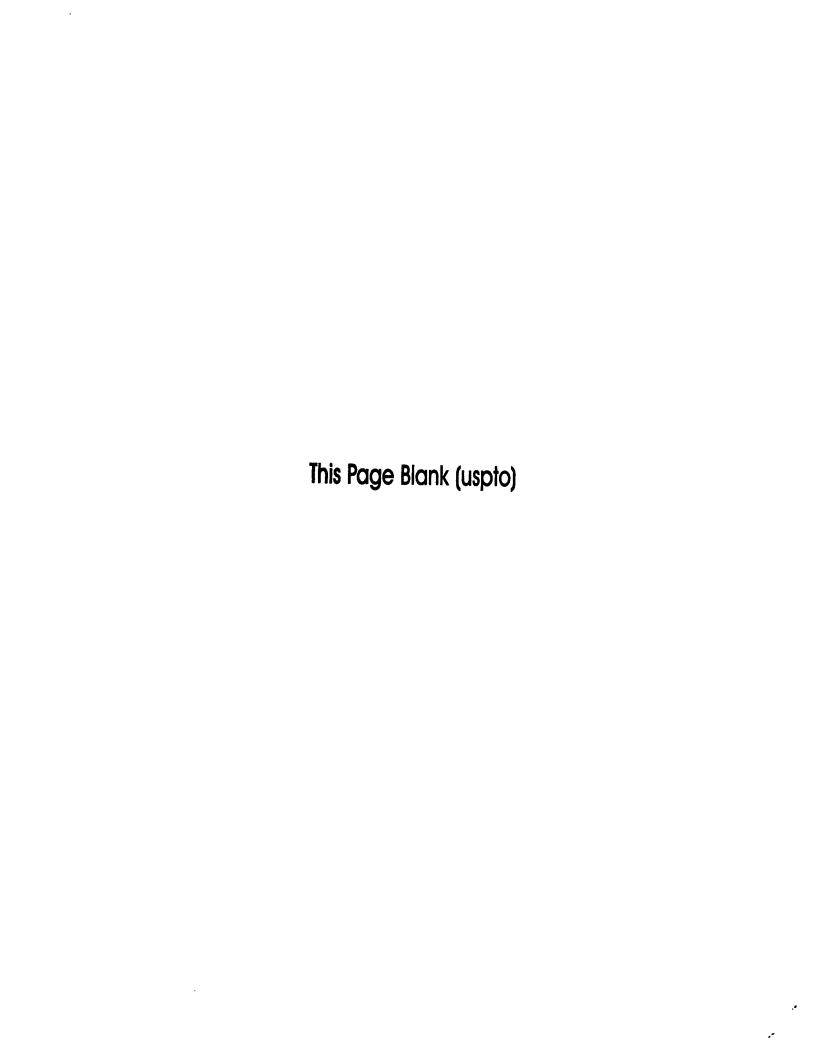
; Sequence 15, Application US/10032162

; Publication No. US20030052839A1

; GENERAL INFORMATION:
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APPLICANT: BINLEY, JAMES M
APPLICANT: SCHUELKE, NORBERT
APPLICANT: OLSON, WILLIAM C
APPLICANT: OLSON, WILLIAM C
APPLICANT: PAUL, MADDON J
APPLICANT: JOHN, MOORE P
TITLE OF INVENTION: STRAILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
FILE REFERENCE: 2044/59331az
CURRENT APPLICATION NUMBER: US/10/032,162
CURRENT PILING DATE: 2002-10-24
PRIOR APPLICATION UNMBER: 09/602,864
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SSO ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Gaps
                                                                                                                                                                                                                                                                                                                                                  Query Match
83.3%; Score 2771; DB 14; Length 579;
Best Local Similarity 85.6%; Pred. No. 2.7e-245;
Matches 529; Conservative 16; Mismatches 31; Indels 42
                                                                                                                                                                                                                                                          ; LENGTH: 579
; TYPE: RTT
; OGGANISM: Human immunodeficiency virus type 1
US-10-032-162-15
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Search completed: February 25, 2004, 14:28:11 Job time : 34.2957 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein February 25, 2004, 14:12:55; Search time 17.6158 Seconds (without alignments) 3380.063 Million cell updates/sec Run on:

US-09-891-609A-4 3327 1 SAVEKLWVTVYYGVPVWKEA......DKWASLWNWFDISKWLWYIK 619 Title: Perfect score: Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         | 1 4    | env poryprocern pr | envelope glycopiot | enverope grycopioc | processi | polyprotein |        |        | env polyprotein pr | env polyprotein pr | _      | env polyprotein - | env polyprotein - | env polyprotein pr |        |        |        |        | envelope polyprote | envelope polyprote | env polyprotein pr |        | env polyprotein pr | envelop glycoprote | env polyprotein M | env polyprotein P | env polyprotein D | env polyprotein - | envelope protein p |
|---------------------|--------|--------------------|--------------------|--------------------|----------|-------------|--------|--------|--------------------|--------------------|--------|-------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|
| SUMMARIES           | UAAOO1 | 10044              | 919614             | 21328              | VCLAA2   | VCLJH3      | VCLJLV | 833985 | VCLJVL             | VCLJSC             | S13288 | VCLJBR            | VCLJH4            | VCLJKX             | VCLJKB | VCLJ3W | VCLJMN | VCLJZR | T01672             | 554384             | A44963             | VCLJND | VCLJSI             | A40218             | A41621            | C41621            | B41621            | S31493            | 849197             |
| DB                  | ::-    | ۱ ،                | 4 0                | 4 (                | ٠,       | · ~         | Н      | ~      | Н                  | Н                  | N      | Н                 | Н                 | Н                  | Н      | Н      | Н      | Н      | N                  | ~                  | Н                  | -      | -                  | N                  | N                 | N                 | ~                 | ~                 | 7                  |
| Length              | 9      | 0 7 0              | 0 0                | 8 6 6              | 855      | 856         | 861    | 851    | 856                | 861                | 854    | 852               | 898               | 729                | 861    | 856    | 859    | 855    | 859                | 823                | 856                | 846    | 854                | 206                | 445               | 443               | 454               | 495               | 877                |
| &<br>Query<br>Match |        |                    |                    |                    | 20.00    | 85.7        | 85.6   | 85.3   | 85.3               | 85.2               | 85.1   | 84.7              | 84.6              | 83.9               | 83.9   | 83.8   | 83.3   | 77.9   | 77.7               | 77.3               | 76.4               | 76.2   | 62.9               | 59.2               | •                 | 58.4              | 55.6              | 'n.               | 54.2               |
| Score               | 3000   | 9000               | 2000               | 0.000              | 2856     | 2851        | 2848.5 | 2839.5 | 2838               | 2836               | 2830   | 2817              | 2813.5            | 2792.5             | 2792.5 | 2787.5 | 2772.5 | 2593   | 2583.5             | 2571               | 2540.5             | 2534.5 | 2191               | 1969.5             | 1945.5            | 1941.5            | 1849              | 1839              | 1803               |
| Result<br>No.       | -      | • 0                | ۹ ۳                | ۰ ۹                | יטי      | φ           | 7      | 80     | σ                  | 10                 | 11     | 12                | 13                | 14                 | 15     | 16     | 17     | 18     | 19                 | 20                 | 21                 | 22     | 23                 | 24                 | 25                | 26                | 27                | 28                | 29                 |

275

216 IRSENFTDNAKTIIVQLKBSVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAHCN

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| gag polyprotein - | env protein - huma | envelope polyprote | env polyprotein pr | env polyprotein pr | env polyprotein - | envelope polyprote | envelope polyprote |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| A53034            | S25940             | S60538             | 860528             | S60545             | S60524             | 860529             | S60548             | S60546             | S60547             | 860521             | VCLJGG             | VCLJST             | C46356            | 860532             | 860531             |
| ٠.                |                    |                    | ~                  | ~                  | a                  | ß                  | a                  | ~                  | ۰.                 | ~                  |                    |                    | ~                 | ۰.                 | 7                  |
| (V                | N                  | N                  | •••                |                    |                    |                    |                    | •••                | •••                | •••                | _                  | _                  | ٠.                | . 4                |                    |
| 863 2             | 290 2              | 297 2              | 299                | 294                | 294                | 299                | 301                | 300                | 300                | 299                | 852 1              | 859                | 877               | 301                | 301                |
| _                 | 39.1 290 2         | •                  | •                  |                    | ••                 | •••                | •                  |                    |                    | •                  | _                  | _                  | _                 |                    |                    |
| 51.7              |                    | 38.7               | 35.7               |                    | 35.7               | 35.6               | 35.4               | 35.3               | 35.2               | 35.1               | 35.1               | 35.0               | 35.0              | 35.0               | 35.0               |

## ALIGNMENTS

| - | RESULT 1   |   |
|---|--|---|
|   | env polyprotein precursor - human in<br>N.Alternate names: coat polyprotein                        | env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2) Alternate names coat polyprotein                                |
|   | N) Contains: coat protein gpizo; (S) Species: human immunodeficien A:Note: host Homo saniens (man) | Nýcontains: coat protein gpiro; coat protein gp41<br>C;Species: human immunodeficiency virus type 1, HIV-1<br>A:Note: host Homo sanians (man) |
|   | C;Date: 31-Dec-1993  | C.D. C. 1.25  |
|   | R;Li, Y.; Hui, H.; B   | Rill, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  |
|   | A; Title: Complete nu  | J. Virol. 66, 6587-6600, 1992<br>A,Title: Complete nucleotide sequence, genome organization, and biological properties of                     |
|   | A; Accession: H44001   | A44001; MUID:93021387; PMID:1404605   |
|   | A, Molecule type: DNA  |   |
|   | A;Residues: 1-843 <liy><br/>A;Cross-references: GB:M93258</liy>                                    | IY><br>GB:M93258  |
|   | C, Genetics:   |   |
|   | A; Gene: env   | A. Gunder and D. France D. Marketting Comp. and Landbook Comp.  |
|   | C; Keywords: cype  | C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  |
|   | F;1-29/Domain: signa   | l sequence #status predicted <sig></sig>  |
|   | F:30-489/Product: CO   | 115-5-5) Kegiou: nyutojiobic<br>F:30-489/brodict: coat profesi mol20 #status predicted «GPI»  |
|   | F;490-843/Product: C   |   |
|   | F:499-515/Region: hydrophobic  | drophobic<br>drophobic  |
|   | F;738-755/Domain: tr   | F;738-755/Domain: transmembrane #status predicted <tmn></tmn>   |
|   | F;87,129,135,138,154   | F;87,129,136,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435,   |
|   | Query Match  | 87.3%; Score 2906; DB 1; Length 843;  |
|   | Matches 544; Con   | ative 3   |
|   | Oy 1 SAVEKL  | SAVEKLWTTVYYGVPVWKEATTTLFCASDAKAYDTSVHNVWATHACVPTDPNPQEIVLEN 60   |
|   | DD 28 SAAEQL   | SAAEQLWVIVYYGVPVWKEATITIFCASDAKAYDTEVHNVWATHACVPTDBNPQEVKLEN 87   |
|   | Qy 61 VTENFN   | VTENFNMWKNIMWEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEM 120  |
|   | OD 88 VIENFN   | SLWDQSLKPCVKLTPLCVTLNCTDLRNATNTT  |
|   | Qy 121 DRGEIK  | DRGEIKNCSFKVGAGKLINCNTSVITQACPKVSFE 155   |
|   | :<br>    Db  | ::        <br>EKGEIKNCSFNITTSIRDKVQKEYALFYNLDVVPIDNASYRLISCNTSVITQACPKVSFE 207  |
|   | Qy 156 PIPIHY  | PIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVV 215  |
|   |  |   |

us-09-891-609a-4.rpr

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CiAccession: T12006
RimColuchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hun. Retroviruses 14, 329-337, 1998
Airtiele Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in Standersence number: Z17379; MUID:9817816; PMID:9519894
A;Reference number: Z17379; MUID:9817816; PMID:9519894
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Status: 1-852 <MCC>
A;Cross-references: EMBL:U90934; NID:92351783; PIDN:AAC59271.1; PID:92351784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 VIENFNIMWKNIMVEQMHEDIISLWDQSLKPCVKLTPLCVTLANCTDYLRNDTNTTSNNGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTN-LKNATNTKSSNWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 EVVIRSENFTDNAKTIIVQLNESVEINCTRPNNNTRKSIHIGPGQALYATGAIIGDIRQA
NSTW-NNTIGPNNTNG-TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLT
                                                                                              RDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVT
                                                                                                                        LGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK
                                                                                                                                                                                                                         512 -LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWERE
                                                                                                                                                                                                                                                                                                                           566 QLQARVLAVERYLGDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDRIWNNMTWMEWERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 SAAEQLRUTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDFNPQEVVLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 SFEPIPIHYCTPAGFALLKCKDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQA
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                                                                                                                                                                                                                                                                                                                                                                                           2; Length 852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 87.2%; Score 2900.5; DB 2; Local Similarity 84.3%; Pred. No. 3.7e-202; hes 552; Conservative 32; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: env
C,Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coverage glycoprotein - human immunodeficiency virus type 1 (strain JRFL)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Space: 16-0M1-1999 #sequence_revision 16-0M1-1999 #text_change 24-Nov-1999

C;Pace: 16-0M1-1999 #sequence_revision 170948

R;Pang, S: Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, Bubminted to the EMBL Data Library, July 1996

A;Reference number: Z16673

A;Reference number: Z16673

A;Accession: T09448

A;Accession: T0
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                                                                                                                                                                           - TWNDTRKLNNTGRNITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDG 445
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                                                   276 ISGEKWNNTLKQIVTKLQAQFG-NKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFN 334
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                                                                               GKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVVQREKRAVTLGA
                                                                                                                                                                                                                                                                                                                                                  MFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIK-LQ
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87.3%; Score 2906; DB 2;
Best Local Similarity 85.4%; Pred. No. 1.5e-202;
Matches 554; Conservative 25; Mismatches 38;
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|-------------------------------|--|---|
| \$ 93                         | 446 EKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQL 505<br>      :              ::  | CY 571 IDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619  |
| රු දු                         | 506 TVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTW 564   | RESULT 5<br>. VCLJA2  |
| cy<br>B                       | 565 MEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619<br>  | env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2) N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence revision 17-May-1985 #text change 16-Jul-1999 |
| RESULT<br>S13289              | RESULT 4<br>\$13289<br>env brottein - human immunodeficiency virus tyme 1  | C;Accession: A03976 R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi Science 227, 484-492, 1988 A: Hitle: Mirlartide seminance and contraction of an AIDS_associated retroving (ADV_2)   |
| C;Speci<br>C;Date:            |  | A;ILLE: NULLECTURE SEQUENCE AND EXPLESSION OF AN ALIX-ASSOCIACED FELLOVILUS (ANY-2). A;Accession: A04003; MUID:85090453; PMID:2578227 A;Accession: A03076 A:Accession: A04003   |
| R;O'Bri<br>Nature<br>A;Title  | Zack, J.A<br>of gp120  | A;Residues: 1-855 <san><br/>A;Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666<br/>C;Genetics:</san>  |
| A;Refer<br>A;Acces<br>A;Statu |  | A;Gene: env<br>C;Superfamily: type E retrovirus env polyprotein<br>C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote  |
| A,Molec<br>A,Resid<br>C,Super |  | F;1.30/Domain: signal sequence #status predicted <sig><br/>F;31-50/Product: exterior membrane glycoprotein #status predicted <ext><br/>F;510-855/Product: transmembrane glycoprotein #status predicted <tmma< td=""></tmma<></ext></sig>  |
| Query<br>Best                 |  | F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458,<br>F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted  |
| Match<br>Oy                   | les 551; Conservative 24; Mismatches 42; Indels 32; Gaps 6; 1 SAVEKLWVIVYXGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDFNDQEIVLEN 60                | Query Match 85.8*; Score 2856; DB 1; Length 855; Best Local Similarity 82.3*; Pred. No. 6.2e-199; Matches 540; Conservative 32; Mismatches 46; Indels 38; Gaps 6;   |
| q <sub>0</sub>                | 28 SATEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLEN 87   | VEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN 60   |
| <u>ک</u> ج                    | 61 VTENFNAMKNINVEQMHEDIISLMDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEM 120  | Db 28 SATEKLWTVTYGVPVWKEATTTLFCASDARAYDTEVHNVWATHACVPTDPNPQEVVLGN 87  Cv 61 VTFNPNMAKNNMVFOMHEDITSLWDOSLYPCVKLTPLCTNLKNATNTKSSNMYFRM 120  |
| ` &                           | DRGEIKNCSFKVGAGKLINCNTSVITQACPKVS  | 88 VIENFNAMKANAVEQAQEDIISLADQSLKFCVKLTFLCVTLACTDLGKATNTNSSNAKEE   |
| qa                            | FIGETINITIESTRDEVQKEYALFYKLDVVPIDNNTSYRLISCDTSVITGACPKIS   | 121 DRGEIKNCSFKVGAG   |
| g g                           | 154 FEPTPIHYCAPAGFALLKCNDKKFNGSGPCTNVSTYQCTHGIRPVVSTQLLLNGSLAEEG 213<br>207 FEPIPIHYCAPAGFALLKCNDKTFNGKGPCKNVSTVDCTHGIRPVVSTQLLLNGSLAEEE 266 | Db 148 IKGEIKNCSFNITTSIRBKIQKENALFRNLDVVPIDNASTTTNYTNYRLIHCNRSVITQA 207  Qy 149 CPKVSFEDIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLAGS 208  |
| ò                             | 214 VVIRSENFTDNAKTIIVQLKESVEINCTRPNNTRKSITIGPGRAFYATGDIIGDIRQAH 273  | Db 208 CPKVSFEDIPIHYCTPAGFALLKCNNKTFNGKGFCTNVSTVQCTHGIRPIVSTQLLLNGS 267   |
| ብ <i>&amp;</i>                | 267 VVIRSDNFTNNAKTIIVQLKESVEINCTRPNNNTRKSIHIGBGRAFYTTGEIIGDIRQAH 326<br>274 CNISGEKMNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF 333 | Qy 209 LAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGD 268   |
| QQ                            |  | 269 IRQAHCNISGEKMNNTLKQIVTKLQAQFG-NKTIVFKQSSGGDPEIVMHSFNCGGEFFYC  |
| <u>ئ</u> ۾                    | 334 NSTW-NNTIGPNNTNG-TITLPCRIKQIINRWOEVGRAMYAPPIRGQIRCSSNITGLLLI 391   | IVK   |
| l &                           | RDGGKEI SNTTEI FRECGGDMRDNWRSELYKYKVVKI BPLGVAPTKAKRVVQREKRAVT   | 388 NITQLFNNTWRLAHIEGTKG-NDTIILPCRIKQIINMWQBVGKAMYAPPIGGGISCSSNI  |
| A 5                           | 447 PIGGIN-ENGTEIFREGGEDREDWRSELYKKYVKIEDLGVAPITARTVOREKRVVOREKRAG 505   | Qy 386 TGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQR 445   |
| · 음                           |  | 446 EKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLO  |
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William polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-la)

NyAlternate names: coat polyprotein
Cispecies: human immunodeficiency virus type 1, HIV-1
A,Note: human immunodeficiency virus type 1, HIV-1
A,Note: human immunodeficiency virus type 1, HIV-1
A,Note: host Homo saplens (man)
Cibate: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
CiAccession: A03975
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85093131; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>A;Accession: A03975
A;Coss-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C;Genetics:
A;Gene: env
C;Genetics:
A;Gene: env
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; fatatus predicted <EXT>
F;1-30/Domain: signal sequence #status predicted <EXT>
F;1-130/Domain: signal sequence #status gredicted <ITWM>
F;81-661/Product: transmembrane glycoprotein #status predicted <ITWM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                     999
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                               OLTVWGIK-LOARVLAVERYLKDOOLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM
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Cipate: 1, Fags, 1985 #Bequence_revision 1, Fagy 1985 #tex__change 10 Jul. 1999
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A9353; MUID:8511123; PMID:2578615
C;Genetics: A;References: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C;Genetics: A;Gene: env
C;Genetics: A;Gene: exterior membrane glycoprotein; immunodeficiency; polyprot F;1-30/Domain: signal sequence #status predicted <816-
F;1-30/Domain: signal sequence #status predicted <816-
F;1-11/Product: exterior membrane glycoprotein #status predicted <FMM>F;81-2856/Product: transmembrane glycoprotein #status predicted <FMM>F;81-2856/Product: transmembrane glycoprotein #status predicted <FMM>F;81-1156,160,186,197,230,234,241,262,276,289,295,330,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Bainding site: carbohydrate (Asn) (covalent) #status predic
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                                 563
                                                              88
                                                                                                                                                                                                                                                                            env polyprotein precursor - human immunodeficiency virus type 1 (isolate HT N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #sequence_revision 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999 R;Ratner, L.; Haseltine W. n....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                           C.Species: human immunodeficiency virus type 1
C.Species: human immunodeficiency virus type 1,
C.Species: S33985
R.Carlini, F.
Submitted to the EMBL Data Library, November 1991
A.Reference number: S33979
A.Reference number: S33985
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-851 < CAR>
A.Residues: 1-851 < CAR>
A.Residues: 1-851 < CAR>
A.Coss-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C.Superfamily: type E retrovirus env polyprotein
                                        IRCSSNITGLLLTRDGGNN-NNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKA
                                                                             QQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQ
                                                                                                                               IWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWY
                                                                                                                                             SATEKLAVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVN
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enu polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

Cispecies: human immunodeficiency virus type 1 (isolate LV)

Cispecies: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C;Accession: A03974

R;Mussing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.

Nature 313, 450-458, 1985

A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovin A;Reference number: A93355; MUID:85111157; PMID:2982104

A;Rocession: A03974

A;Rocession: A03974

A;Rocession: A03974

A;Rocession: A03974

A;Rocession: A03974

A;Rocession: A03974

C;Genetics: A;Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559

C;Genetics: A;Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559

C;Genetics: A;Genetics: A;Genetic
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C.Superienty: and S. Capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F.1-10/Domain: signal sequence #status predicted <SIG>
F.1-15/Domain: signal sequence membrane glycoprotein #status predicted <EXT>
F.512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F.512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F.88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,312,339,356,386,392,397,406,
F.611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
565
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506 RAVGIGALFLGFLGBAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTV
                                                                                                                                      120 MDRGEIKNCSFKVGA---GK----------LINCNTSVITQACPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 EVVIRSANPIDNAKTIIVQINQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGK-IGNWR
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                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                 567 WEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
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determined by regions of gp120 c
                                                                                                                                                                                                                                                           env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13288
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, v. Nature 349, 69-73, 1990
Nature 349, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl: A;Reference number: S13288; MUD:91043044; PMID:2172833
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                                                           567 QQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICTTTVPWNTSWSNKSLKD
                                                                                                                       1 SAVEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2830; DB 2;
Pred. No. 4.8e-197;
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-854 <OBR
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Matches 542
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NyAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Home sapiens (man)
C;Date: 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Reference number: A28922
A;Molecule type: DNA
A;Residues: 1-861 cGUR>
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/Domain: signal sequence #status predicted cEPP>
F;30-861/Product: env polyprotein #status predicted cEPP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,366,396
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82.3%; Pred. No. 1.8e-197;
iive 30; Mismatches 43;
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N. Alternate names: coat polyprotein
N. Alternate names: coat polyprotein
N. Contains: coat protein gp120; coat protein gp41
C. Species: human immunodeficiency virus type 1, HIV-1
A. Youce: host Homo sapiens (man)
C. Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C. Accession: A31667
R. Andrew R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S. Tanicoby 168, 79-89, 1989
Virology 168, 79-89, 1989
A.Title: Biological and molecular characterization of human immunodeficiency virus (HIV-A-Reference number: A94389; MUID:89085613; PMID:2789516
A. Residues: 1-852 < ANA-Speciesion: A3167
A. Residues: 1-852 < ANA-Speciesion: A3167
A. Residues: 1-852 CANA-Speciesion: Polyprotein (C. Keywords: capsid protein; polyprotein; transmembrane protein C. Keywords: capsid protein; gp41 #status predicted < CP1-Species Product: coat protein gp41 #status predicted < CP2-Species CP2-Species CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP2-Species CP3 Product: coat protein gp41 #status predicted < CP3-Species CP3 Product: coat protein gp41 #status predicted < CP3-Species 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFNSTWYRNTIG-NITEGNSPITLPCRIKQIINMWQEVGKAMYAPPIRGQIKCSSNITGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWME
VTENFNMWKNNMVEQMHEDI I SLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLTRDGGKEISNT-TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAVGLGALFLGFLGAAGSTMGAASLTLTVQARLLLSGIVQQQNNLLMAIEAQQHMLELTV
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                                                                                                           MEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                             env polyprotein - human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.7%; Score 2817; DB 1;
81.6%; Pred. No. 4.1e-196;
iive 38; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRGEI KNCSFKVGAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.6
Matches 533; Conservative
                                                                                     265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
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Allernate names: coat polyprotein

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Mar-1996

C;Accession: A42995

R;Shimizu, H.; Haeebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

R;Shimizu, H.; Haeebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

R;Shimizu, H.; Haeebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

R;Shimizu, H.; Haeebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virology 189, 534-546, 1992

A;Reference number: A42995; MUID:9215152; PMID:132287

A;Recension: A42995

A;Recension: A42995

A;Recension: A42995

A;Recension: A2296

A;Recension: A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSL 209
                                                                                                                                           498
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                                         QQHLLQLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQ
                                                                                                                                                                                                                                                                                                                            SNITGLLLTRDGGKEISNTT----EIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPTKA
                                                                                                                                           KRRVVQREKRAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                      558 IWNNMTWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQBIVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72/Region: hydrophobic #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 79.3%
Matches 525; Conservative
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C;Superfamily: type E retrovirus env polyprotein;
C;Superfamily: coat protein; glycoprotein; polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-33/Domain: signal sequence #status predicted <EXT>
F;1-33/Domain: signal sequence #status predicted <SIG>
F;17-31/Region: hydrophobic #status predicted <CP1>
F;18-517/Product: coat protein gp32 #status predicted <CP2>
F;18-517/Region: cleavage processing #status predicted <CP2>
F;18-53/Region: hydrophobic #status predicted <CP2>
F;18-53/Region: hydrophobic #status predicted <IN1>
F;19-729/Domain: transmembrane #status predicted <IN1>
F;112-729/Domain: intracellular #status predicted <IN1>
F;112-1145,146,163,191,192,237,241,248,269,283,296,308,338,335,361,367,397,403,408,414
                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: coat polyprotein manuodeficiency virus type 1 (strain KB-1-gp32)
NyAlternate names: coat polyprotein
NyAlternate names

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - KGEIKNCSFNVTTNIRDKVQKEYALFYKLDVVPIDNDNNSTNTCYRLISCDTSVITQAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKVSFEPIPIHYCTPAGFALLKCNNKTFNGTGPCKNVSTVQCTHGIRPVVSTQLLLNGSL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOLFNST-----WINTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCS 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTENFUMWKUNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKEM 120
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                                         624 ASWSNKTLDQIWNNNTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELQLDLWASLWT 683
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A,Molecule type: mRNA
A,Residues: 1-729 <SHI>
A;Cross-references: GB:S41266; GB:D01206
C;Genetics:
A;Gene: env
                                                                                                                                                      608 WFDISKWLWYIK 619
                                                                                                                                                                                            684 WSDITKWLWYIK 695
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Matches 525; Conservative
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        QY
        210 ABEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDI
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        DD
        273 AEGGVVIRSENFTDNAKTIIVQLAFTURINCIRPNNKTRKRVTMGFGRYYTTGEIIGDI
        332

        QY
        270 RQAHCNISGERMNTILKQIYTKLQAQFGNKTIVFRQSSGGDPEIVMHSFNCGGEFYCDS
        329

        QY
        313 TQLENST------WINTIGPNNTRGTITLPCRIKQIINRWQEVGRAWYAPPIRGQIRCS
        347

        DD
        393 SQLFNSTHLSNGTWWNGTI-GPENKTIVFNQSSGGDPEIVMHFNCGGEFYCDS
        392

        QY
        330 TQLENST-----WINTIGPNNTRGTITLPCRIKQIINRWQEVGRAWYAPPIRGQIRCS
        447

        DD
        393 SQLFNSTHLSNGTWWNGT-GPEN----ITLPCRIKQIINRWQEVGRAWYAPPIRGQIRCS
        447

        QY
        383 SNTTGLLLTRDGGKEISNTT-----IFRPGGGBMRDWWSSELYKKVVXIEPLGVAPTRA
        507

        QY
        448 SNTTGLLLTRDGGKEISNTT------IFRPGGGBMRDWWSSELYKKVVXIEPLGVAPTRA
        507

        QY
        439 KRRVVQREKRAVGIGAVFLGFLGAAGSTWGARSLLTLTVQARQLLSGIVQQNNLLRAIDA
        507

        QY
        499 QQHLLQLTVWGIK-LQARVLGTAGSTRGARSLTTLTVQARQLLSGIVQQNNLLRAIDA
        567

        QY
        499 QQHLLQLTVWGIK-LQARVLGTAVERYLKDQQLAGIWGSCGCLICTTAVPWNTSWSNKSFNB
        57

        QY
        558 IWNNWTWMBWEREINNYTNLLYNLIESQNQQEKNEQDLLALDKWASCHYLKTRUMY
        67

        CD
        628 IWNNWTWMBWEREINNYTNLLYNLIESGQNQQEKNEQDLLALDKWASCHYLKTWWWGITTRWWY
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        CD
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Copyright (c) 1993 - 2004 Compugen Ltd.
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        ENV_EVSTA
        P18040 human immun

        35
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        38
        1165.3
        34.9
        768
        1
        ENV_SIVAL
        P2757 simian immun

        39
        1162.5
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        1
        ENV_HVZGA
        P2757 simian immun

        40
        1139.5
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        859
        1
        ENV_HVZCA
        P05883 human immun

        41
        1129
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        1
        ENV_HVZBE
        P05886 simian immun

        42
        1129
        33.9
        860
        1
        ENV_HVZBE
        P18094 human immun

        44
        1126.5
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        ENV_HVZBE
        P18094 human immun

        45
        1115
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        ENV_HVZBC
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Best Local Similarity 95.2%;
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RESULT 2 ENV\_HV1Y2 ID\_ ENV\_HV1Y2

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1G9N; 27-DEC-00.
InterPro; IRR000328; Env GP41.
InterPro; IRR000377; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
                                                                                                                                                                                                                                          "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation."; J. Virol. 66:6587-6600(1992).
          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1904 (Rel. 42, Last annotation update)
Envelope polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
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POTENTIAL.
BY SIMILARITY.
BY SIMIL
                                                                                                         Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1) Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=36377;
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PRR, H44001; H44001.
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MEDLINE=93021387; Pubmed=1404605;
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                                                                                                SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                               Gaps
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ENV HV1SC

AC P05878; 856 AA.

DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last amoutation update)
DR Revelope polyprotein GP160 precursor [Contains: Exterior membrane GN ENV.
(POTENTIAL).
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                                                                               30;
                                                             Length 843;
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                                                                               35; Indels
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MEDLINE-88219542; Pubmed-3369091;
Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (SC isolate) (HIV-1)
Viruses, Retroid viruses, Retroviridae, Lentivirus.
                 -LINKED (GLCNAC. . .) (PO-LINKED (GLCNAC. . .) (PO-LINKED (GLCNAC. . .) (PO-C69DFD971C918B71 CRC64;
                                                           87.3%; Score 2906; DB 1;
84.2%; Pred. No. 1.5e-217;
tive 37; Mismatches 35;
(GLCNAC.
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598 N-
603 N-
612 N-
624 N-
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95648 MW;
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843 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
-!- MISCELLANBOUS: THE SC ISOLATE WAS TAKEN PROM AN ARC PATIENT IN
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TRANSMEMBRANE GLYCOPROTEIN.
IN PRAME TERMINATION CODON.
BY SIMILARITY.
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EXTERIOR MEMBRANE GLYCOPROTEIN.
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TRANSMEMBRANE GLYCOPROTEIN.
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BY SIMILARITY.
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Pred. No. 1.5e-215;
1; Mismatches 40;
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HIV; M17450; ENV$SC.
InterPro; IPR0003738; ENV GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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Best Local Similarity 83.3
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147 ERGEIKNCSFNITKSIRDKVQKEYALFYKLDVVPIDNKNNTKYRLISCNTSVITQACPKV
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HIV; M38429; ENV$JRCSF.
InterPro; IPR000328; ENV GP41.
InterPro; IPR000777; GP1\overline{\text{GP}}0.
Pfam; PF00516; GP41; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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                                                                                                                                                          EXTERIOR MEMBRANE GLYCOPROTEIN.
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                                                                                     VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLK-----NATNTKSS
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      SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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01-FBB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein (91100 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Submitted (DEC-1988) to the HIV data bank.
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PDB; 1CE4; 18-MAR-99.
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148 IKGEIKNCSFNITTSIRDKIQKENALFRNLDVVPIDNASTTTNYTNYRLIHCNRSVITQA
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82.3%; Pred. No. 1.2e-213;
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                      FINSTWINTIGPUNITIG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLL
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MEDLINE=85090453; PubMed=2578227;
Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
Levy J.A., Dina D., Luciw P.A.;
"Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                    619
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11685;
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PIR; A03976; VCLJA2.
HIV; K02007; ENV$SF2.
HIV; K02007; ENV$SF2.
InterPro; IPR000777; GP120.
Pfam; PF00515; GP120; 1.
Pfam; PF00517; GP120; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
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Matches 548; Conservative 3
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                                                                       626
                       566
              EKRAVGIVGAMFLGFLGAAGSTMGAVSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQ
                                                            LTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMT
                                                                                                WMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                             SEQUENCE FROM N.A.

BEDLINE-SB111123 PubMed=2578615,
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Bauneister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T.,
Wong-Staal F.,
                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP12)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90285159; PubMed=2355006; Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.; Intrachain disulfide bonds and characterization of nassignment of intrachain sites of the type 1 recombinant human immunodefliciency virus envelope glycoprotein (gpl20) expressed in Chinese hamster ovary cells."; J. Biol. Chem. 265:10373-10382(1990).
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HIV; MIS654; EVV$HH102.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
A1DS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
Signal.
GHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
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TRANSMEMBRANE GLYCOPROTEIN.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
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                                                                                                                                                                                      STANDARD;
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82.8%; Pred. No. 4.5e
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QLTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNM 562
                                                     TWMEWEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
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BMBL; A04321; CAA00352.1; -.

PIR; A03975; VCLJLV.

PDB; IERF; 20-FEB-02.

HIV; K02013; ERV$BRU.

InterPro; IPR00077; GP120.

Pfam; PF0516; GP120; 1.

Pfam; PF0511; GP41; 1.

Pfam; PF0517; GP41; 1.

AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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P03377;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP91)].
                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (BRU isolate) (HIV-1)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11686;
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MEDLINE=85099333; PubMed=2981635;
Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
"Nucleotide sequence of the AIDS virus, LAV.";
Cell 40:9-17(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 VSTQLLLNGSLAEEEVVIRSENFTDNVKTIIVQLNASVQINCTRPNNNTRKSITKGPGRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 FYATGDIIGDIRQAHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVWHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 SAAEDLWVTVYYGVPVWKEATTTLFCASEAKAYKTEVHNVWAKHACVPTDPNPQEVLLEN
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                     (POTENTIAL).
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80.3%; Pred. No. 2.5e-212;
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ENV_HV1PV
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Matches 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-86218077, PubMed=2423250;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf Starcich B.R., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
"Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."
                                                                                                                                                                                                                                                                                                                                  membrane
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TRANSMEMBRANE GLYCOPROTEIN.
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InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
1 29
                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1) Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GPL60 precursor [Contains: Exterior mglycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                                                                                                                                                                                                                                        29 SATEKLMVTVYYGVPVMKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVN
                                                                                                                                                                                                                                                                                                                                                                                     61 VTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 SFEPIPIHYCAPAGFALLKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 EVVIRSANFTDNAKTIIVQLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGK-IGNMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 QAHCNISRAKWNWTLKQIDSKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 TOLFNSTWAN----TIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS
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                                                                                                                                                                                                                                                                                                 1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 TOLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKOFINMWQEVGKAMYAPPISGOIRCSS
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P04578; 009779;
13-AUG-1997 (Rel. 05, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP41)].
                         ..) (POTENTIAL).
..) (POTENTIAL).
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                                                                                                                                                                                                                                                    40;
       (POTENTIAL)
                                                                                                                                                                                                          Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGCB_TaxID=11706;
611 N-LINKED (GLCNAC. . . ) (POTE 616 N-LINKED (GLCNAC. . . ) (POTE 625 N-LINKED (GLCNAC. . . ) (POTE 637 N-LINKED (GLCNAC. . . ) (POTE 674 N-LINKED (GLCNAC. . . ) (POTE 674 N-LINKED (GLCNAC. . . ) (POTE 750 N-
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                       Score 2838; DB 1;
Pred. No. 2.9e-212;
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              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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TRANSNEMBRANE GLYCOPROTEIN.
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Coat protein; Polyprotein; Glycoprotein; Transmembrane;
                                                                                                                                                      Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11700;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=85111157; PubMed=2982104;
Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Capon D.J.;
                                                                                                                                                                                                                                                                                                                                        expression of the human
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EMBL; X01762; CAA25903.1; ALT_SEQ.
PIR, A03974; VCLVI...
HIV; K02083; ENVSPV2...
InterPro; IPR000128; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00516; GP41; 1.
AIDS; Coat protein; Polyprotein; Gly
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Nature 313:450-458(1985).
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AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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      MEDLINE-87299196; PubMed=1040055; Ratner L., Ritsuya H., Liou R.-S., Ratner L., Rishber A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F. a. "Complete nucleotide sequences of functional clones of the AIDS
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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EMBL; AF03839; AAB9976.1; --
EMBL; AF03819; AAC82596.1; --
EMBL; DF4; Z6-JAN-00.
PD8; IDF5; Z6-JAN-00.
PD8; IDF5; Z6-JAN-00.
PD8; IG9M; Z7-DEC-00.
PD8; IGC1; 19-AUG-98.
PD8; IGZL; 10-OCT-01.
PD8; IX34; IO-OCT-01.
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BNV HV1B8

AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane DE glycoprotein (GP120); Transmembrane glycoprotein (GP120); Transmembrane glycoprotein (GP12)
                                   (POTENTIAL) .
(POTENTIAL) .
(POTENTIAL) .
(POTENTIAL) .
(POTENTIAL) .
(POTENTIAL) .
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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SEQUENCE FROM N.A.
MEDLINE=8511123; PubMed=2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.(Wong-Staal F.)
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                                                     "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1985).
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TRANSMEMBRANE GLYCOPROTEIN.
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96644 MW;
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                                                                                             1 SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                                                                                              SATEKLWYTVYFGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVN
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MEDLINE-89085613; PubMed-2789516;
Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
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P12488;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GPL60 precursor (Contains: Exterior membrane glycoprotein (GPL20); Transmembrane glycoprotein (GPL20);
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Length
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11693;
                                              Indels
                                                 41;
$; Score 2829.5; DB 1;
$; Pred. No. 1.3e-211;
33; Mismatches 41;
Query Match
Best Local Similarity 83.0%;
Matches 542; Conservative 3
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446 388

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447

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                                                                                                                                                                                                                                                           WGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWME 566
89 VTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCHDF-NATNATSNSGKMM 147
                                               -----KLINCNTSVITQACPK 151
                                                                                                                                                                : ||:||||| :
EGGEMKNCSFNITTSIRDKMQKEYALFYKLDIVPIDNDKTNTRYRLISCNTSVITQACPK
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MEDLINE=90148544; PubMed=2559749;

Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S

Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S

"A highly defective HIV-1 strain isolated from a healthy Gabonese
individual presenting an atypical western blot.";

Alborous S. T. - 15 (1889).

- 1- MISCELLANBOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A

HEALTHY GABONESE INDIVIDUAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
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Ol-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior nglycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11699;
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR0003128; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AlDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
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PIR; A31667; VCLJBR.
PDB; 11M7; 23-OCT-02.
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                                                                                                                                                      568 TVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTTVPWNASWSNKSLNEIWDNMTW
                                CNSTOLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNIT
                                                           GLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQRE
                                                                                                                                                                                                                    KRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQL
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences."; Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11687;
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Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
Andersen P.R., Devare S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus type 1.";
AIDS Res. Hum. Retroviruses 6:371-380(1990).
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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HIV, M13137; ENV$CDC45.
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                       MYAPPIRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIE
                                                                                                             PLGVAPTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQ
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Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
Shaw G.M., Wong-Staal F., Reddy B.P.;
"Hard-III env gene products synthesized in E. coli are recognized h
antibodies present in the sera of AIDS patients.";
Cell 41:979-986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENV HV1H3 STANDARD; PRT; 856 AA.
P04624;
13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP41)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1) Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11707;
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TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
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InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP20; 1.
Pfam; PF00517; GP41; 1.
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Query Match:
84.4%; Score 2808; DB 1; Length 856;
Best Local Similarity 82.3%; Pred. No. 6.2e-210;
Matches 541; Conservative 33; Mismatches 43; Indels 40; Gaps 10;

|   | SAVEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVFTDFNFQEIVLEN 60<br> | VTENFNAMKANAWEQWHEDIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTKSSNWKE-119<br> | MDRGEIKNCSFKVGAGK | SPEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEE 212<br> | GVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIR 270<br> | OAHCNISGEKWNNTLKQIVTKLQAQFG-NKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNS 329<br> | TQLFNSTWNNTIGPNNTNGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSS 383<br> | NITGLLLTRDGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVV 443<br> | Orekrautigamfigfigaagstmgarsltituvqarqilisgivqqqnnilraibaqhil 503 |
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BMBL; AF536757; AAN05642.1; -.
GO; GO:001993; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000177; GP41.
InterPro; IPR000177; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP120; 1.
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STRAIN=81NJ;

MEDLINE=22628496; PubMed=12743293;

MEDLINE=22628496; PubMed=12743293;

MEDLINE=22628496; PubMed=12743293;

MCObins K.E., Lemey P., PyDus O.G., Jaffe H.W., Youngpairoj A.S.,
Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;

"U.S. Human Immunodeficiency Jiros Type 1 Epidemic: Date of Origin
Population History, and Characterization of Early Strains.";

J. Virol. 77:6359-6366[2003].

EMBL; AX247221; AAP37149.1; -.

Envelope protein:
SEQUENCE 850 AA; 96583 MW; 62ED5F6AB033D20B CRC64;
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86.2%; Pred. No. 1e-233;
ive 24; Mismatches 33; Indels
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Last sequence update)
Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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  VVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQAH
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MEDLINE-22684946;

Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,

Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;

Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;

U.S. Human Immunodeficiency Virus Type I Epidemic: Date of Origir

Population History, and Characterization of Early Strains.";

J. Virol. 77:6359-6366(2003).

BRIL, AY27222;

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EKGEIKNCSFNITTNIRDKMQKEYALFYRLDVVPIDNDSTNTSYRLISCNTSVITQACPK
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EMBL; AX247220; AAP37148.1; -
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85.6%; Pred. No. 2.2e-233;
ive 24; Mismatches 35; Ir
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
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SEQUENCE 852 AA
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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84.4%; Pred. No. 1.9e-233;
.ive 27; Mismatches 35;
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01-OCT-2003 (TrEMBLrel.
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SEQUENCE FROM N.A.
STRAIN=014;
MEDLINE=95194691; PubMed=7545977;
MEDLINE=95194691; PubMed=7545977;
WHO Global Programme on AIDS;
"HIV type 1 variation in World Health Organization-sponsored vaccine evaluation sites; generic screening, sequence analysis, and preliminary biological characterization of selected viral strains. WHO Network for HIV Isolation and Characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gao F., Yue L., Craig S., Thornton C.L., Robertson D.L., McCutchan F.E., Bradac J.A., Sharp P.M., Hahn B.H.; "Genetic variation of HIV type 1 in four World Health Organization-sponsored vaccine evaluation sites: generation of functional envelope (glycoprotein 160) clones representative of sequence subtypes A, B, C, and E. WHO Network for HIV Isolation and Characterization."; AIDS Res. Hum. Retroviruses 10:1359-1368(1994).
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EGGEIKNCSFNITTSLRDKMQKEYALFYKLDVVPIDNDNTNTSYRLISCNTSVITQACPK
                                                                                                                         VSFEBIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVOCTHGIRPVVSTOLLLNGSLAE
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                ------KLINCNTSVITQACPK
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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MEDLINE=95194694; PubMed=7888189;
                                                               DRGEIKNCSFKVGAG------
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BIMBL, AY247219, AAP37147.1; -. ERVELOPE PROTECTION AS SEQUENCE 853 AA, 96545 MW; E3B2830A1261E237 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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    562 OLOARVLAVERYLKDOOLLGIWGCSGKLICTTAVPWNASWSNKSLDKIWNNMTWMEWERE 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction and characterization of a stable full-length macrophage tropic HIV type 1 molecular clone that directs the production of high titers of progeny virions.";
AIDS Res. Hum. Retroviruses 12:191-194(1996).
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4CB 854 AA; 97291 MW; 06C45E69103C6C12 CRC64;
                                                           571 IDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK
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Submitted (WAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF004391, C.integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
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01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07N-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI TaxID=11676;
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87.9%; Score 2924.5; DB 1:
Best Local Similarity 85.1%; Pred. No. 7.2e-230;
Matches 558; Conservative 17; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTWMEWERE 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KLINCNTSVITQACPKVSF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGGEIKNCSFNITTSIKTKVKDYALFYKLDVVPIDNDNTSYRLINCNTSVITQACPKVSF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIPIHYCTPAGFAILQCNNKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRSSNPTDNARVIIVQLMESVEINCTRPNNNTRKSIHLGPGRAWYTTGQIIGDIRQAHC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISGEKWINTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLFN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STWNNTIGPNNT--NGTITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTR 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAV-T 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                      "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. The WHO and NIAID Networks for HIV Isolation and Characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAVEKLWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 843;
                                                                       MEDLINE=96190564; PubMed=8627686;
Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig &
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                         Allen E.E.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases EMBL; U08801; AB05105.1; -.
GO; GO:00106021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
R GO: GO:005198; F:structural molecule activity; IEA.
R InterPro; IPR000773; GP120.
R Pfam; PF00516; GP120; 1.
R Pfam; PF00516; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 87.9%; Score 2925; DB 15; Local Similarity 84.9%; Pred. No. 6.5e-230; Hes 551; Conservative 25; Mismatches 39;
Res. Hum. Retroviruses 10:1327-1343(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            843 AA; 95679 MW;
                                                                                                                                                                                                                                  J. Virol. 70:1651-1657(1996)
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                                    SEQUENCE FROM N.A.
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                                                       STRAIN=014;
                                                                                                                                                      Hahn B.H.;
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SEQUENCE
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208 FEPIPIHYCAPAGFAILKCKDKKFDGKGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEE 267
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                                                                                                                                                                                                                                      388 NSTWNDTEGSNDTERTITLPCRIKQIINWWQKVGKAMYAPPIRGQIRCSSNITGLLTRD
                                                                                                                                                                                                                                                                                                                           GGKEISNTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVTLG
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                                                                                                                             CNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQLF
                                                                                                                                                                                                                NSTWINTIGPINITIGITLEPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNITGLLLTRD
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bull infection of the central nervous system by AIDS viruses with
distinct cellular tropisms.";
Science 236:819-822(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pang S., Vinters H.V., Akashi T., O'Brien W.A., Chen I.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pang S., Vinters H.V., Akashi T., O'Brien W.A., Chen I.S.; "HIV-1 env sequence variation in brain tissue of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related neurologic disease.";
J. Acquir. Immune Defic. Syndr. 4:1082-1092(1991).
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01-NOV-1996
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                                                                                                                                                                                                                                             FNSTWN-----NTIGPNNTNG--TITLPCRIKQIINRWQEVGKAMYAPPIRGQIRCSSNI 385
                                                                                                                                                                                                                      EKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQ 504
                                                                                                                                                                                                                                                                                                            LTVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMT 563
  CNISRTKWNNTLNQIATKLKEQFGNNKTIVFNQSSGGDPEIVMHSFNCGGEFFYCNSTQL 385
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EKGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDNNSTRYRLISCNTSVITQACPKVT
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                                                                       TGLLLTRDGGKEISNTTEIFRPGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQR
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                            WMEWEREIDNYTHLIYTLIEESONQOEKNEGELLELDKWASLWNWFDISKWLWYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of HIV1-PAR, a macrophage-tropic strain: cell tropiem, virus/cell entry and nucleotide sequence of the envelope glycoprotein.";
Res. Virol. 144:21-26(1993).
Res. Virol. 144:21-26(1993).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019021; C:viral envelope; IEA.
InterPro; IPR000328; Estructural molecule activity; IEA.
InterPro; IPR000377; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-93189881; PubMed-8446773;
Schmidtmayerova H., Gayet O., Guettari N., Bolmont C., Hirsch I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.6%; Score 2914.5; DB 15; Length 846; 84.7%; Pred. No. 4.7e-229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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PF00517; GP41; 1.
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ERGEIKNCSFNITTSIRDEVQKEYALFYKLDVVPIDNNNTSYRLISCDTSVITQACPKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDNYTSEIYTLIEESQNQQEKNEQELLELDKWASLWNWFDITKWLWYIK 674
                                                                                                                                                               87.3%; Score 2906; DB 15; Length 847;
85.4%; Pred. No. 2.3e-228;
ive 25; Mismatches 38; Indels 32
                                                                                                                               AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 847 AA; 96160 MW; 022D5F24E04FB29F CRC64;
A Koyanagi Y., Namazie A., Zhao J., Diagne A., Idler K.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. R EMBL, 103632, AAB05604.1; -. PPR 18. 513289; S13289. R PIR, 109448; T09448 T09448. T09448. T09481 T09488. T095189. Sincepral to membrane; IEA. GO; GO:0015028; C:viral capsid; IEA. GO; GO:0015198; F:structural molecule activity; IEA. R InterPro; IPR000128; Bnv GP41. R InterPro; IPR000128; Bnv GP41. R InterPro; IPR000179; GP120. R Pfam; PF00516; GP120; 1. R Pfam; PF00517; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 EVVIRSENFTDNAKTIIVQLNESVEINCTRPNNNTRKSIHIGPGQALYATGAIIGDIRQA 327
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                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN=scl4.3;

MEDLINE=sel14.3;

WASHINE=sel14.3;

WASHINE Res. Hum. Retroviruses 14:329-337(1998).

WASHINE ASIS91: ASIS91:

WASHINE ASIS91: ASIS91:

WASHINE TIZO16; TIZO16;

WASHINE TIZO1
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                                     viruses; Retroviridae; Lentivirus
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87.2%; Score 2900.5; DB 15
Best Local Similarity 84.3%; Pred. No. 6.6e-228;
Matches 552; Conservative 32; Mismatches 32;
Human immunodeficiency virus 1.
                                  Viruses; Retroid
NCBI_TaxID=11676;
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507 EKRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARLLLSGIVQQQNNLLRAIEAQQHLLQL 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPIPIHYCAPAGFALLKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEGV
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                                                                                                   1 SAVEKLWYTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIVLEN
                                                                     TVWGIK-LQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNMTW
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Sheppard W.H.;

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Third T
                                                                                                                                                                                                MEWERBIDNYTNLIYTLIEBSQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619
                                                                                                                                                                                                                                  Length 851;
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851 AA; 96516 MW; 1CDAC83EE6464531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SFWHSB.1;
MEDLINE=98178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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83.1%; Pred. No. 1.8e-227
ive 36; Mismatches 40
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A WEDLINE-91289160; PubMed=1905842;

A Hwang S.S., Boyle T.J., Lyerly H.K., Cullen B.R.;

I'dentification of the envelope V3 loop as the primary determinant of cell tropism in HY-1.";

IL Science 253:71-74(1991).

IR Science 253:71-74(1991).

R GO; GO:0019021; C:integral to membrane; IEA.

R GO; GO:0019022; C:viral capsid; IEA.

R GO; GO:0019028; C:viral envelope; IEA.

R GO; GO:0019028; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.

R InterPro; IPR000371; GP120.

R Pfam; PF00517; GP120; 1.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Pred. No. 1.7e-227;
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Matches 546; Conservative
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         SFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLABE
                                                                                             GVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIGDIRQA
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"Diversity of the human immunodeficiency virus type 1 envelope
"Diversity of the human immunodeficiency virus type 1 envelope
glycoprotein in San Francisco Men's Health Study participants.";
ALDS Res. Hum. Retroviruses 14:329-337(1998).
BEMBL, AR025751; AAC40589.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019023; C:intagral capsid; IEA.
GO, GO:0019031; C:viral capsid; IEA.
GO, GO:005198; F:structural molecule activity; IEA.
InterPro; IRR000328; Env GP41.
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NCE 853 AA; 96830 MW; EC8BA4418F8AEC47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SFWHS3.1;
MEDLINE=98178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
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Last annotation update)
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NCBI_TaxID=11676;
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ilarity 84.2%; Pred. No. 2.7e-227;
Conservative 24; Mismatches 45;
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01-JUN-2003 (TrEMBLrel.
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Pfam; PF00517; GP41; 1
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NCE 854 AA; 97287 MW; AFD8A82B62C5B27D CRC64;
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MEDLINE=98178716; PubMed=9519894;
McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Pfam; PF00517; GP41; 1
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| VTENFNRWKANRWVEQMHEDIISLWDQSLKPCVKLJFLCVTLHCT-NLKARINTKSSNWKE 119<br> | MDRGEIKNCSFKVGAG               | KVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLA 210<br> | EGOVVIRSENFTDNAKTIIVQLKESVEINCTRPNNTRKSITIGPGRAFYATGDIIGDIR 270 | ORHCNISGEKWNNTLKQIVTKLQAQFGNKTIVFKQSSGGDPEIVWHSFNCGGEFFYCNST 330<br> | OLFNSTWINTIGENNTNGTITLPCRIKOLINRWGEVGKAMYAPPIRGOIRCSSNITG 387<br> | LLLTRDGGKEISNTTEIFRPGGGDMRDMMRSELYKKKVVKIEPLGVAPTKAKRRVVQREK 447<br> | RAVTLGAMFLGFLGAAGSTMGARSLTLTVQARQLISGTVQQQNNLLRAIEAQQHLLQLTV 507<br>    :  : | WGIK-LQARVLAVERYLKDOQLLGIWGCSGKLICTTAVPWNASWSNKSLDOIWNNFFWME 566<br> | WEREIDNYTNLIYTLIEESQNQQEKNEQELLELDKWASLWNWFDISKWLWYIK 619<br> |
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| VTENFNMW<br>        <br>VTENFNMW                                      | MDRGEIKO<br>      <br>EMRGEIKO | KVSFEPIF<br>        <br>KVSFEPIF                                     | EEGWIRS   | QAHCNISG<br>     : <br>QAHCNLSR                                      | OLFNSTWN<br>        <br>OLFNSTWN                                  | LLLTRDGG<br>        <br>LLLTRDGG                                     | RAVTLGAN<br>    :  :<br>RAVGIGAN   | WGIK-LOP<br>        <br>WGIKQLOP                                     | WEREIDNY<br>        <br>WEREIDNY                              |
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